OM protein - protein search, using sw model

Run on: January 6, 2005, 19:40:10 ; Search time 191 Seconds
(without alignments)
1042.302 Million cell updates/sec

Title: US-10-041-859-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAAATLVMLKN............TDKCPMCRRTFTNAVRLYFS 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1887	100.0	346	2	Q96T8	Q96t8 bombyx mori
2	1866	98.9	346	2	Q8I931	Q8i931 bombyx mori
3	1327	70.3	379	2	Q9U492	Q9u492 trichoplusi
4	1311	69.5	375	2	Q9NJ07	Q9nj07 spodoptera
5	966	51.2	277	1	IAP_GVCP	Iap_gvcp
6	937	49.7	287	2	Q6E7G7	Q6e7g7 anticarsia
7	890.0	47.2	280	2	Q6VTV9	Q6vtv9 choristoneu
8	890.5	47.2	280	2	AAQ91688	Aaq91688 choriston
9	879	46.6	263	2	Q80SF4	Q80sf4 hyphantria
10	876	46.4	281	2	Q9YNL8	Q9ynl8 choristoneu
11	873	46.3	281	2	Q90ES9	Q90es9 epiphyas po
12	873	46.3	276	2	O89744	O89744 buzura supp
13	862	45.7	268	1	IAP3_NPVOP	Iap3_npvop
14	782	41.4	264	2	Q9EN27	Q9en27 amsacta moo
15	747.5	39.6	255	2	Q7T5S1	Q7t5s1 cryptophleb
16	728	38.6	289	2	Q7QJ55	Q7qj55 anopheles g
17	728	38.6	313	2	Q9J827	Q9j827 spodoptera
18	723.5	38.3	438	2	IAP1_DROME	Iap1_drome drosophila
19	719.5	38.1	438	2	Q9VUX5	Q9vux5 drosophila
20	701	37.1	403	2	Q8WRD9	Q8wrd9 aedes trise
21	684	36.2	401	2	Q6Q507	Q6q507 aedes aegyp
22	684	36.2	401	2	AA566751	Aa566751 aedes aeg
23	676.5	35.9	402	2	Q8T621	Q8t621 aedes albop
24	662	35.1	285	2	Q8JM16	Q8jm16 mamestra co
25	653	34.6	276	2	Q71A73	Q71a73 mamestra co
26	653	34.6	276	2	Q8QL95	Q8ql95 mamestra co
27	653	34.6	276	2	AAQ11158	Aaq11158 mamestra
28	635	33.7	283	2	Q80LK8	Q80lk8 adoxophyes
29	573	30.4	254	2	Q7T9J6	Q7t9j6 adoxophyes
30	544.5	28.9	269	2	Q6QXJ6	Q6qxj6 agrotis seg
31	544.5	28.9	269	2	AAS82685	Aas82685 agrotis s
32	542	28.7	358	1	Q9EZ32	PIAP_PIG O62640 sus scrofa
33	532.5	28.2	268	2	Q9Z32	Q9232 helicoverpa
34	530.5	28.1	401	2	Q8JHV9	Q8jhv9 xenopus lae
35	529.5	28.1	268	2	Q71LW6	Q71lw6 helicoverpa
36	529.5	28.1	268	2	Q71fw6	Q71fw6 helicoverpa
37	528.5	28.0	602	2	Q91f18	Q91f18 helicoverpa
38	526.5	27.9	604	1	BIR3_HUMAN	Q9ese9 rattus norv
39	525.5	27.8	600	1	BIR3_MOUSE	Q13489 homo sapien
40	520.5	27.6	604	1	O89863	Q6dy3 mus musculu
41	516.5	27.4	616	2	Q6DY3	Q804e2 xenopus lae
42	513.5	27.2	604	2	Q804E2	Q6gld7 xenopus tro
43	513	27.2	628	2	Q6gld7	Q8uwd2 ictalurus p
44	513	27.2	647	2	Q8uwd2	Q7t0k2 xenopus tro
45	513	27.2	654	2	Q770K2	Q62m93 brachydanio
					Q62m93	brachydanio

RESULT 1

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Q96T8
ID   Q96T8        PRELIMINARY;  PRT;   346 AA.
AC   Q96T8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Inhibitor of apoptosis protein.
GN   Name=IAP;
OS   Bombyx mori (Silk moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC   Bombycidae; Bombyx.
OX   NCBI_TaxID=7091;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21240184; PubMed=11341966;
RA   Huang Q., Deveraux Q.L., Maeda S., Stennicke H.R., Hammock B.D.,
RA   Reed J.C.;
RT   "Cloning and characterization of an inhibitor of apoptosis protein
RT   (IAP) from Bombyx mori.";
RL   Biochim. Biophys. Acta 1499:191-198(2001).
DR   EMBL; AF281073; AAK57560.1; -.
DR   HSSP; Q24306; 1JD4.
DR   GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006916; P:anti-apoptosis; IEA.
DR   GO; GO:0016567; P:protein ubiquitination; IEA.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR008841; Znf_ring.
DR   Pfam; PF00653; BIR; 2.
DR   SMART; SM00238; BIR; 2.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 2.
DR   PROSITE; PS01283; BIR_REPEAT_2; 2.
DR   PROSITE; PS50143; BIR_REPEAT_2; 1.
DR   PROSITE; PS50089; ZF_RING; 1.
SQ   SEQUENCE   346 AA;  38942 MW;  6CFC6C6468894C69 CRC64;
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ALIGNMENTS

```
Q96T8

Query Match         100.0%;  Score 1887;  DB 2;  Length 346;
Best Local Similarity  100.0%;  Pred. No. 1e-149;
Matches  346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 MELTKVAKNGAAATLVMLKNARDAKMRPFIGPLMLSSCESSTTSTLPSPSSSADKTDNHD   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MELTKVAKNGAAATLVMLKNARDAKMRPFIGPLMLSSCESSTTSTLPSPSSSADKTDNHD   60

Qy   61 TFNFLPDMPDMRREEERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCCAFCKVEIMRW  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TFNFLPDMPDMRREEERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCCAFCKVEIMRW  120

Qy  121 VEGDDPAADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAAATQPPRMPGPVHARYS  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 VEGDDPAADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAAATQPPRMPGPVHARYS  180
```

[handwritten annotation: JANIS]

```
Qy  181 TEAARLATFKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKDWESDDVPWEQHA 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TEAARLATFKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKDWESDDVPWEQHA 240

Qy  241 RWFDRCAYVQLVKGRDYIQKVKSEATAISASEEEQAATNDSTKNVAQEGEKHLDDSKICK 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 RWFDRCAYVQLVKGRDYIQKVKSEATAISASEEEQAATNDSTKNVAQEGEKHLDDSKICK 300

Qy  301 ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS 346
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Db  301 ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS 346
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```
RESULT 2
ID   Q8IS31      PRELIMINARY;   PRT;   346 AA.
AC   Q8IS31;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Inhibitor of apoptosis protein.
OS   Bombyx mori (Silk moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC   Bombycidae; Bombyx.
OX   NCBI_TaxID=7091;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yang G., Wang L., Wu X.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY155274; AAN46650.1; -.
DR   HSSP; Q24306; 1JD4.
DR   GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006916; P:anti-apoptosis; IEA.
DR   GO; GO:0016567; P:protein ubiquitination; IEA.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; znf_ring.
DR   Pfam; PF00653; BIR; 2.
DR   SMART; SM00238; BIR; 2.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 2.
DR   PROSITE; PS50143; BIR_REPEAT_2; 2.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE  346 AA;  38849 MW;  5450EB75F56A8486 CRC64;
```

```
Query Match         98.9%;  Score 1866;  DB 2;  Length 346;
Best Local Similarity  99.1%;  Pred. No. 6e-148;
Matches  343;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy    1 MELTKVAKNGAAATLVMLKQNARDAKMRPFIGPLMLSSCESSSTTSTLPSPSSSADKTDNHD 60
        |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    1 MELTKVAKNGAAATLVMLKNARDAKMRPFIGPLMLSSCESSSTTSTLPSPSSSADKTDNHD 60

Qy   61 TFNFLPDMDMRREEERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCCAFCKVEIMRW 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TFNFLPDMDMRREEERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCCAFCKVEIMRW 120

Qy  121 VEGDDPAADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAAATQPPRMPGPVHARYS 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 VEGDDPAADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAAATQPPRMPGPVHARYS 180

Qy  181 TEAARLATFKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKDWESDDVPWEQHA 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TEAARLATFKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKDWESDDVPWEQHA 240

Qy  241 RWFDRCAYVQLVKGRDYIQKVKSEATAISASEEEQAATNDSTKNVAQEGEKHLDDSKICK 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 RWFDRCAYVQLVKGRDYIQKVKSEATAISASEEEQAATNDSTKNVAQEGEKHLDDSKICK 300

Qy  301 ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS 346
        ||||||||||||||||||||||||||||||||||||||||||||||
Db  301 ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS 346
```

```
Db  301 ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS 346
        ||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 3
ID   Q9U492      PRELIMINARY;   PRT;   379 AA.
AC   Q9U492;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Inhibitor of apoptosis protein.
GN   Name=IAP1;
OS   Trichoplusia ni (Cabbage looper).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC   Noctuidae; Plusiinae; Trichoplusia.
OX   NCBI_TaxID=7111;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20062908; PubMed=10593985;
RA   Seshagiri S., Vucic D., Lee J., Dixit V.M.;
RT   "Baculovirus-based genetic screen for antiapoptotic genes identifies a
RT   novel IAP.";
RL   J. Biol. Chem. 274:36769-36773(1999).
DR   EMBL; AF195528; AAF19819.1; -.
DR   HSSP; Q24306; 1JD4.
DR   GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006916; P:anti-apoptosis; IEA.
DR   GO; GO:0016567; P:protein ubiquitination; IEA.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; znf_ring.
DR   Pfam; PF00653; BIR; 2.
DR   SMART; SM00238; BIR; 2.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 2.
DR   PROSITE; PS50143; BIR_REPEAT_2; 2.
DR   PROSITE; PS50089; ZF_RING_2; 1.
SQ   SEQUENCE  379 AA;  41857 MW;  0693BIA012D9DB65 CRC64;
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Query Match         70.3%;  Score 1327;  DB 2;  Length 379;
Best Local Similarity  69.0%;  Pred. No. 9.8e-103;
Matches  251;  Conservative  39;  Mismatches  54;  Indels  20;  Gaps  8;

Qy    1 MELTKVAKNGAAATLVMLKQNA--RDAKMRPFIGPLML---SSCESSSTTSTLPSPSS------ 51
        :|:|||   || :  || ||||||||      ||| |||:|||||||
Db   18 MDITKVASNGPASPLTLFKNAPRDAKIRPLV-PLVLPTQSYDSNAGSPASSPSTPSSSSSS 76

Qy   52 -SADKTDNHDTFNFLPDMDMRREEERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCC 110
        :| |||||||:||:     | ||| ||| :|||||||||||||||||||||||||
Db   77 FSIDKTDNHDTFSLTADAVDMSREDERIKTFEKWPVSFLSGEQLARNGFYYLGRGDEVRC 136

Qy  111 AFCKVEIMRWVEGDDPAADHRRWAPQCPFVRK-LGGGVNTDSGAARGPYYLGRGDEVC 168
        |||||||||||||||||| |:|| |||||||||    ::
Db  137 AFCKVEIMRWVEGDDPAKDHQRWAPQCPFVRK-LGGGVNTDSGAAGRDECGARAAPTSSP 195

Qy  169 PRMPGPVHARYSTEAARLATFKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKD 228
        ||||||:|||: ||||||  ||||||: ||||||||||||||||||||||||||||||||
Db  196 SRMPGPVHPRYASEAARLRSFKDWPRCMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKD 255

Qy  229 WESDDVPWEQHARWFDRCAYVQLVKGRDYIQKVKSEATAI----SASEEE---QAATNDST 282
        ||:||||||| |:   ||||||| ||::  ||| :  :    :|||||    :
Db  256 WENDDVPWEQHARWFDRCAYVQLVKGREYVQKWMTEACVIPAPAAPRDEAPARSAAEPSV 315

Qy  283 KNVAQEGEKHLDDSKICKICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVR 342
        :|:   |  :|:||||  |||  |||||||||||||||||||||:  ||:||||||:  ||
Db  316 VSAAEPQESTLDDSKLCKICFAEERNVCFVPCGHVVACAKCALAADKCPMCRRTFQNAVR 375

Qy  343 LYFS 346
        ||||
Db  376 LYFS 379
```

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: January 13, 2005, 13:40:00

Title: US-10-041-859-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAAATLVMLKN............TDKCPMCRRTFTNAVRLYFS 346

Run on: January 13, 2005, 13:40:00
                (without alignments)
                1873.146 Million cell updates/sec
                ; Search time 6731 Seconds

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0
                Delop 6.0 , Delext 7.0

Searched: 3822875 seqs, 1821986908 residues

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Total number of hits satisfying chosen parameters: 65445750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Command line parameters: -DEV=xlh
-MODEL=frame+_p2n.model
-Q=/cgn2_1/USPTO_spool/US10041859/runat_10012005_155634_27790/app_query.fasta_1.519
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000000
-USER=US10041859 @CGN 1 1 3437 @runat_10012005_155634_27790 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=-0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST.*
            1: gb_est1.*
            2: gb_est2.*
            3: gb_htc.*
            4: gb_est4.*
            5: gb_est5.*
            6: gb_est6.*
            7: gb_gss1.*
            8: gb_gss1.*
            9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Match	Query Length	DB	ID	Description
	1	1053	55.8	712	5	BP121000	BP121000
	2	1053	55.8	727	5	BP120885	BP120885
	3	985	52.2	723	7	AV401669	AV401669
	4	928	49.2	622	7	CK497882	CK497882
	5	861.5	45.7	555	5	BP121882	BP121882
	6	812	43.0	512	1	AV398511	AV398511
	7	684	36.2	510	5	BP115618	BP115618
c	8	647	34.3	804	9	CG786123	CG786123 CM MBa-76
c	9	545	28.9	1288	3	CR688416	CR688416 Tetraodon

RESULT 1
BP121000

LOCUS   BP121000   712 bp   mRNA   linear   EST 16-MAY-2003
DEFINITION BP121000 ceN- Bombyx mori cDNA clone ceN-4016, mRNA sequence.
ACCESSION   BP121000
VERSION   BP121000.1 GI:29554042
KEYWORDS   EST.
SOURCE   Bombyx mori (domestic silkworm)
  ORGANISM Bombyx mori
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
            Bombycoidea; Bombycidae; Bombyx.
REFERENCE   1 (bases 1 to 712)
  AUTHORS   Mita,K., Morinyo,M., Shimada,T., Okano,K. and Maeda,S.
  TITLE   Bombyx mori cDNA (Mita,K. 2003)
  JOURNAL   Unpublished (2003)
COMMENT   Contact: Mita K
            Genome Research Group
            National Institute of Agrobiological Sciences
            Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
            Email: kmita@nias.affrc.go.jp
            method:uni-directional, sequence direction:sequenced from T3 primer
FEATURES   Location/Qualifiers
     source   1..712
                     /organism="Bombyx mori"
                     /mol_type="mRNA"
                     /db_xref="taxon:7091"
                     /clone="ceN-4016"
                     /tissue_type="compound eye"
                     /clone_lib="ceN"
                     /note="mixed stages from 5th instar larva to pupa"
ORIGIN

ALIGNMENTS

	No.	Score	%		Length		Accession	Description
	10	536	28.4	3	1353	3	CR692095	CR692095 Tetraodon
	11	520	27.6	3	1347	3	CR729221	CR729221 Tetraodon
	12	519	27.5	5	522	7	CK516014	rBwjb0_00
	13	514	27.2	5	723	7	C0640316	USDA-FP_1
	14	510.5	27.1	9	1778	9	AY420755	AY420755 Mus muscu
	15	503	26.7	7	2079	7	CR733861	CR733861 Tetraodon
	16	500.5	26.5	4	782	6	CB690915	CB690915 Aede
	17	498.5	26.4	6	712	4	BM601939	170006870
	18	497	26.3	9	1439	3	CR702049	17006870
	19	493.5	26.2	3	1799	9	AY420753	AY420753 Homo sapi
	20	488	25.9	7	2047	3	AY724410	Tetraodon
	21	486	25.8	3	1851	3	BC056914	BC056914 Homo sapi
	22	484	25.8	4	1789	3	BC046168	BC046168 Homo sapi
	23	467	24.7	3	864	5	CK189215	EST778530
	24	453.5	24.0	3	718	3	AY432429	Aedes aeg
	25	446.5	23.7	7	887	7	CN502150	AGENCOURT
	26	446	23.6	6	771	6	CA803224	ESG011a.E
	27	445	23.6	5	727	5	CF525095	AGENCOURT
	28	445	23.6	7	1045	7	CN645252	ILLUMIGEN
	29	440.5	23.3	4	881	6	CF265917	AGENCOURT
	30	437	23.2	7	950	7	CO647969	ILLUMIGEN
	31	435	23.1	5	886	5	BQ552590	AGENCOURT
	32	428	22.7	5	567	4	B1961039	MONO1_5_C
c	33	426.5	22.6	4	678	5	CA805412	MONO1_5_C
	34	426	22.6	7	910	6	CA981958	AGENCOURT
	35	425.5	22.6	5	745	7	CN062644	Ag2_p37_J
	36	425	22.5	4	887	6	BJ728878	BJ728878
	37	423	22.4	6	937	6	CA981608	AGENCOURT
	38	421.5	22.3	7	781	6	CF152602	AGENCOURT
	39	421	22.3	5	1084	5	BU902159	AGENCOURT
	40	420	22.3	4	644	1	AL854961	AL854961
	41	418.5	22.2	3	929	5	CA981777	AGENCOURT
	42	415	22.2	7	586	7	CF913919	AGENCOURT
	43	414.5	22.0	6	857	5	CA985214	AGENCOURT
	44	414	21.9	4	851	4	B1253303	602973538
	45	413.5	21.9	6	909	6	CA981433	AGENCOURT

Alignment Scores:
Pred. No.:
Score: 7.91e-96
Percent Similarity: 1053.00
Best Local Similarity: 99.48%
Query Match: 99.48%
DB: 55.80%

Length: 712
Matches: 192
Conservative: 0
Mismatches: 1
Indels: 0
Gaps: 0

US-10-041-859-2 (1-346) x BP121000 (1-712)

Qy   154 AlaValGlyArgAspGluCysGlyAlaSerAlaAlaThrGlnProProArgMetProGly 173
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GCTGTCGGTAGAGACGAAATGTGGGGCGGCCAGTGCGGGCCACCGAACCTCCCCCGCCCGGC 60

Qy   174 ProValHisAlaArgTyrSerThrGluAlaAlaArgLeuAlaThrPheLysAspTrpPro 193
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCCGTGCACGCGCGGTACTCCACCGAGGCGGCCCGCGGCTCGCCACCTTCAAGGACTGGCCG 120

Qy   194 ArgArgMetArgGlnLysProGluGluLeuAlaGlyPhePheTyrThrGlyGln 213
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGATGTATGGGCCAAAAACCCGAGGAACTGGCAGGGCCCGGATTCTTCTTATACAGGCCAA 180

Qy   214 GlyAspLysThrLysCysPheTyrCysAspGlyTyrGlyLeuLysAspTrpProGluSerAspAsp 233
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGTGACAAAACGAAATGCTTCTATTGCGACGGATGGGGAAAGCGATGAC 240

Qy   234 ValProTrpGluGlnHisAlaArgTrpPheAspArgCysAlaTyrValGlnLeuValLys 253
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GTTCCGTGGGAACAGCACGCCCAGATGGTTCGACCGGTACGTGCAATTGGTGAAA 300

Qy   254 GlyArgAspTyrIleGlnIleLysValLysSerGluAlaThrAlaIleIleSerAlaSerGluGlu 273
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGACGTGACTACATTCAGAAGGTGAAGTCGGAGGCCACTGCGATATCTCGCTAGCGAAGAA 360

Qy   274 GlyGlnAlaAlaThrAsnAspSerThrLysAsnValAlaLeuGlnGluGlyLeuHisLeu 293
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAACAGGCCGCCACCAATGATTCGACTAAGAACGTGCCTAAGAGAGGGCGAGAAACATTTG 420

Qy   294 AspAspSerLysIleCysLysIleCysTyrSerGluGluArgAsnValCysPheValPro 313
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GATGACTCTAAAATATGTAAAATATGTTATTCCGAGGAGCGTAACGTGTGCTTCGTGCCG 480

Qy   314 CysGlyHisValValAlaCysLysSerAlaLeuSerThrAspLysCysProMetCys 333
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCGGCCCACGTGGTGGCGCCAAGTCGGCGCTGTCGACGGACAAGTGCCCGATGTGT 540

Qy   334 ArgArgThrPheThrAsnAlaValAlaArgLeuTyrPheSer 346
          ||||||||||||||||||||||||||||||||||||||||||
Db   541 CGCAGGACGGTTCACGAATCGGGTGCGGCTTCTACTTCTCG 579

US-10-041-859-2 (1-346) x BP120885 (1-712)

RESULT 2
BP120885
LOCUS   BP120885   727 bp   mRNA   linear
DEFINITION   BP120885 ceN- Bombyx mori cDNA clone ceN-3830, mRNA sequence.
ACCESSION   BP120885
VERSION   BP120885.1   GI:29553920
KEYWORDS   EST.
SOURCE   Bombyx mori (domestic silkworm)
ORGANISM   Bombyx mori
             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
             Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
             Bombycoidea; Bombycidae; Bombyx.
REFERENCE   1 (bases 1 to 727)
AUTHORS   Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
TITLE   Bombyx mori cDNA (Mita,K. 2003)
JOURNAL   Unpublished (2003)
COMMENT   Contact: Mita K
             Genome Research Group
             National Institute of Agrobiological Sciences
             Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
             Email: kmita@nias.affrc.go.jp
             method:uni-directional, sequence direction:sequenced from T3 primer

---

FEATURES   Location/Qualifiers
     source   1. .727
                     /organism="Bombyx mori"
                     /mol_type="mRNA"
                     /db_xref="taxon:7091"
                     /clone="ceN-3830"
                     /tissue_type="compound eye"
                     /clone_lib="ceN-"
                     /note="mixed stages from 5th instar larva to pupa"

ORIGIN   (5' -> 3').

Alignment Scores:
Pred. No.:
Score: 8.15e-96
Percent Similarity: 1053.00
Best Local Similarity: 99.48%
Query Match: 99.48%
DB: 55.80%

Length: 727
Matches: 192
Conservative: 0
Mismatches: 1
Indels: 0
Gaps: 0

US-10-041-859-2 (1-346) x BP120885 (1-727)

Qy   154 AlaValGlyArgAspGluCysGlyAlaSerAlaAlaThrGlnProProArgMetProGly 173
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GCTGTCGGTAGAGACGAAATGTGGGGCGGCCAGTGCGGGCCACCGAACCTCCCCCGCCCGGC 60

Qy   174 ProValHisAlaArgTyrSerThrGluAlaAlaArgLeuAlaThrPheLysAspTrpPro 193
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCCGTGCACGCGCGGTACTCCACCGAGGCGGCCCGCGGCTCGCCACCTTCAAGGACTGGCCG 120

Qy   194 ArgArgMetArgGlnLysProGluGluLeuAlaGlyPhePheTyrThrGlyGln 213
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGATGTATGGGCCAAAAACCCGAGGAACTGGCAGGGCCCGGATTCTTCTTATACAGGCCAA 180

Qy   214 GlyAspLysThrLysCysPheTyrCysAspGlyTyrGlyLeuLysAspTrpProGluSerAspAsp 233
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGTGACAAAACGAAATGCTTCTATTGCGACGGATGGGGAAAGCGATGAC 240

Qy   234 ValProTrpGluGlnHisAlaArgTrpPheAspArgCysAlaTyrValGlnLeuValLys 253
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GTTCCGTGGGAACAGCACGCCCAGATGGTTCGACCGGTACGTGCAATTGGTGAAA 300

Qy   254 GlyArgAspTyrIleGlnIleLysValLysSerGluAlaThrAlaIleIleSerAlaSerGluGlu 273
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGACGTGACTACATTCAGAAGGTGAAGTCGGAGGCCACTGCGATATCTCGCTAGCGAAGAA 360

Qy   274 GlyGlnAlaAlaThrAsnAspSerThrLysAsnValAlaLeuGlnGluGlyLeuHisLeu 293
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAACAGGCCGCCACCAATGATTCGACTAAGAACGTGCCTAAGAGAGGGCGAGAAACATTTG 420

Qy   294 AspAspSerLysIleCysLysIleCysTyrSerGluGluArgAsnValCysPheValPro 313
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GATGACTCTAAAATATGTAAAATATGTTATTCCGAGGAGCGTAACGTGTGCTTCGTGCCG 480

Qy   314 CysGlyHisValValAlaCysLysSerAlaLeuSerThrAspLysCysProMetCys 333
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCGGCCCACGTGGTGGCGCCAAGTCGGCGCTGTCGACGGACAAGTGCCCGATGTGT 540

Qy   334 ArgArgThrPheThrAsnAlaValAlaArgLeuTyrPheSer 346
          ||||||||||||||||||||||||||||||||||||||||||
Db   541 CGCAGGACGGTTCACGAATCGGGTGCGGCTTCTACTTCTCG 579

US-10-041-859-2 (1-346) x BP120885 (1-727)

RESULT 3
AV401669
LOCUS   AV401669   723 bp   mRNA   linear
DEFINITION   AV401669 Bombyx mori C108 spinning stage day-0 Bombyx mori cDNA
             clone hes00025 T3, mRNA sequence.
ACCESSION   AV401669
VERSION   AV401669.1   GI:6905321
KEYWORDS   EST.
SOURCE   Bombyx mori (domestic silkworm)
ORGANISM   Bombyx mori
             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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OM protein - protein search, using sw model

Run on: January 6, 2005, 19:48:11 ; Search time 40 Seconds
(without alignments)
832.275 Million cell updates/sec

Title: US-10-041-859-2
Perfect score: 1887
Sequence: 1 MELTKVAXNGAAATLVMLKN...........TDKCPMCRRTFTNAVRLYPS 346

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : PIR.79:*
        1: pir1:*
        2: pir2:*
        3: pir3:*
        4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	966	51.2	275	2	A45679	inhibitor-of-apopt
2	862	45.7	268	2	T10304	inhibitor of apopt
3	862	45.7	268	2	A53989	apoptosis-inhibiti
4	542	28.7	358	2	JC5964	apoptosis inhibito
5	524.5	27.8	604	2	S68449	apoptosis inhibito
6	507.5	26.9	618	2	S68450	apoptosis inhibito
7	501	26.6	497	2	S69545	apoptosis inhibito
8	500.5	26.5	496	2	S68452	apoptosis inhibito
9	497.5	26.4	496	2	S69544	apoptosis inhibito
10	381.5	20.2	292	2	T41772	IAP1 orf27 - Bomby
11	378	20.0	286	2	D36828	orf13 protein - Au
12	369.5	19.6	275	2	T10310	apoptosis-inhibiti
13	362.5	19.2	298	2	JC7568	kidney inhibitor o
14	309	16.4	1447	2	T42628	neuronal apoptosis
15	299	15.8	1232	2	A55478	neuronal apoptosis
16	253	13.4	208	2	T03183	probable apoptosis
17	252.5	13.4	150	2	T28409	ORF MSV248 probabl
18	232	12.3	234	2	T30427	probable apoptosis
19	222.5	11.8	155	2	T30489	apoptosis inhibito
20	220.5	11.7	997	2	T43523	cut17 protein - fi
21	171.5	9.1	308	2	T37474	apoptosis inhibito
22	164.5	8.7	249	2	T41814	IAP2 orf71 - Bomby
23	164.5	8.7	329	2	T28403	ORF MSV242 probabl
24	159.5	8.5	249	2	H72858	apoptosis inhibito
25	156	8.3	236	2	T10343	inhibitor of apopt
26	155.5	8.2	383	2	F96582	hypothetical prote
27	154	8.2	4845	2	T31067	BIR repeat contain
28	149.5	7.9	115	2	B96664	probable RING zinc
29	139	7.4	124	2	T01251	hypothetical prote
30	132.5	7.0	864	2	T01393	apoptosis inhibito
31	131.5	7.0	489	2	S15349	mdm2 protein - mou
32	130	6.9	428	2	T48167	hypothetical prote
33	122.5	6.5	237	2	T5432	hypothetical prote
34	122.5	6.5	823	2	D86165	protein F15K9 [i
35	120	6.4	711	2	C84767	hypothetical prote
36	120	6.4	943	2	S68824	rngB protein, cyto
37	119	6.3	433	2	JC7678	RING finger protei
38	117	6.2	491	2	S24354	p53-binding protei
39	116	6.1	754	2	S35503	finger protein neu
40	115	6.1	401	2	G99824	hypothetical prote
41	115	6.1	529	2	T19204	hypothetical prote
42	115	6.1	337	2	T43341	hypothetical prote
43	114	6.0	372	2	C96631	hypothetical prote
44	113.5	6.0	269	2	T40371	probable zinc fing
45	112	5.9	204	2	T01447	hypothetical prote

ALIGNMENTS

RESULT 1
A45679
inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV
C;Species: Cydia pomonella granulosis virus CpGV
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
A;Accession: A45679
R;Crook, N.E.; Clem, R.J.; Miller, L.K.
J. Virol. 67, 2168-2174, 1993
A;Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.
A;Reference number: A45679; MUID:93188168; PMID:8445726
A;Accession: A45679
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-275 <CRO>
A;Cross-references: UNIPROT:P41436; GB:L05494; NID:g289583; PIDN:AAA43835.1; PID:g28958
A;Note: sequence extracted from NCBI backbone (NCBIN:127014, NCBIP:127015)
C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 51.2%; Score 966; DB 2; Length 275;
Best Local Similarity 59.2%; Pred. No. 3.9e-73;
Matches 171; Conservative 39; Mismatches 55; Indels 24; Gaps 3;

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Qy   68  MPDMRREEBRLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCCAFCKVEIMRWVEGDDPA  127
         |:|:||||||||||.:|:|||||||||.:|:|:||.||:||:|||||||||||||||||
Db    1  MSDIRLEEVRLNTFEKWPVSFLSPETMAKNGFVYLGRSDEVRCAFCKVEIMRWKEGDDPA  60

Qy  128  ADIRRWAPQCPFVRKQMYANAGGEATAVGRDECCASAATQ-------PPRMPGPVHARYS  180
         ||:|||||||:||:||  :|:|||       .:||||.||  .     ...|:.|||.|  :
Db   61  ADHKKWAPQCPFVK------------GIDVCGSIVTTNNIQNTTHDTIIGPAHPKYA  106

Qy  181  TERAARLIATPEKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLIKDWDESDDVPWEQHA  240
         |:|||:|:.|:.|||  ||:|:||||||||||||||||:|||||||||:|||  :|:|||||:
Db  107  HEAARVKSFHNWPRCMKQRPEQMADAGFFYTGYGDNTKCFYCDGGLKDWEPEDVPWEQHV  166

Qy  241  RWFDRCAYVQLVKGRDYIQKVKSEATAI---SASEEEQAAATNDSTKQVVAQEGEKHLDDSK  297
         |||||||||||||||||:||| :||  |:    .|:|:|:     ||:||:|:||  ||||
Db  167  RWFDRCAYVQLVKGRDYVQKVITEACVLPGENTTVSTAAPVSEPIPETKIEKEPQVEDSK  226

Qy  298  ICKICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS  346
         :||||| ||.:|||||||||||||||||:.|||||||:::|:.:|||:|
Db  227  LCKICYVEECIVCFVPCGHVVACAKCALSVDKCPMCRKIVTSVLKVYFS  275
```

RESULT 2
T10304
inhibitor of apoptosis protein 3 - Orgyia pseudotsugata nuclear polyhedrosis virus
C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C;Accession: T10304
R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosi

```
A;Reference number: 217011; MUID:97271300; PMID:9126251
A;Accession: T10304
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-268 <AHR>
A;Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59034.1; PID:g1911281
C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F;217-261/Domain: RING finger homology <RRN>

Query Match          45.7%; Score 862; DB 2; Length 268;
Best Local Similarity 54.5%; Pred. No. 1.8e-64;
Matches 150; Conservative 31; Mismatches 72; Indels 22; Gaps 2;

Qy    70 DMRREEERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCCAFCKVEIMRWVEGDDPAAD 129
         | | |:| |||||||||||||||||||||||||||||||||||:||||||||
Db    14 DMKNKAARLGTYTNWPVQFLEPSRMAASGFYYLGRGDEVRCAFCKVEITNWVRGDDPETD 73

Qy   130 HRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAATQPPRMPGPVHARYSTEAARLATF 189
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    74 HKRWAPQCPFVRNNAHDTPHDRA-----------------------PPARSAAAHPQYAT 118

Qy   190 KDWPRMRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKDWESDDVPWEQHARWFDRCAYV 249
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   119 AEWPRGLKQRPEELAEAGFFYTGQGDKTKCFCCDGGLKDWEPDDAPWQQHARWYDRCEYV 178

Qy   250 QLVKGRDYIQKVKSEATAISASEEQAATNDSTKNVAQEGGKHLDDSKICKICYSEERNV 309
         ||:|:|||:|  ::| |||:
Db   179 LLVKGRDFVQRVMTEACVVRDADNEPHIERPAV------------------EAEVADDRLCKICLGAEKTV 231

Qy   310 CFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLY 344
         ||||||||||||||||||||||||||||||||||
Db   232 CFVPCGHVVACGKCAAGVTTCPVCRGQLDKAVRMY 266
```

RESULT 4
JC5964
apoptosis inhibitor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
A;Reference number: JC5964
A;Title: Cytokine induced expression of porcine inhibitor of apoptosis protein (iap) fa...
R;Stehlik, C.; de Martin, R.; Binder, B.R.; Lipp, J.
Biochem. Biophys. Res. Commun. 243, 827-832, 1998
A;Accession: JC5964
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-358 <STE>
A;Cross-references: UNIPROT:O62640; GB:U79142; NID:g2957174; PIDN:AAC39171.1; PID:g29571
F;307-351/Domain: RING finger homology <RRN>

```
Query Match          28.7%; Score 542; DB 2; Length 358;
Best Local Similarity 28.7%; Pred. No. 1.3e-37;
Matches 111; Conservative 47; Mismatches 89; Indels 140; Gaps 5;

Qy    71 MRREEERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCCAFCKVEIMRWVEGDDPAADH 130
         |:||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db     1 MNTEKDRLLTFDQWPWPLTFLSPADLAKAGFYYIGPGDRVACFACGGKLSNWEPKDDAMTEH 60

Qy   131 RRWAPQCPFVRKQMYANAGGEATAVGRDECGASAATQPPRMPGPVHARYS-------TEA 183
         ||||||||||| :|||  ||||||| | | :| | :|| ||| |:  |:  ::     |
Db    61 LRHFPNCPFLIGNQLQDS-------------------------------SRYTVSNLSMQTYA 91

Qy   184 ARLATFKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKDWESDDVPWEQHARWF 243
         |  ||| | ||::|:| |||||||||||||||||||||||||||:|| |   ||:|||||
Db    92 ARFKTFCNWPSSIPVHPEQLASAGFYYMGHSDDVKCFCCDGGLRCWESGDDPWVEHAKWF 151

Qy   244 DRCAYVQLVKGRDYIQKVKSE--------ATAISASEEQAATND----------- 280
         |:| |: :| : : :| ||:       | :|||:||:| |
Db   152 PRCEYLIRIKGQEFISRVQASYPHLLEQLLSTSDNPEDENAEPPNDLSLIRKNRMALFQH 211

Qy   281 --------------------------------------STKNVA----QEGEKHLDDSKICKICYSEERNVCFVPCGHVVA 319
                                                |:||:    ||||:|||||:|||||||:|||||||||||||
Db   212 LTCVLPILDSLLIARVISEQEHDVIKQKTQTSLQARELIDILLVKGNYAATIFKNSLQEI 271

Qy   320 CAKCALSTDKCPMCRRTFTNAVRLYFS 346
         ||:| ||||:|||:||||:|||||:|||
Db   272 DPMIYKHLFVQQDIKYIPTENVSDLSMEEQLRRLQEERTCKVCMDKEVSIVFIPCGHLVV 331

Qy   332 CKDCAPSLRKCPICRGTIKGTVRTFLS 358
         ||| ||| ||||||| ||| :| ||
Db   332 CKDCAPSLRKCPICRGTIKGTVRTFLS 358
```

RESULT 5
S68449
apoptosis inhibitor hiap-1 - human
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
A;Accession: S68449
R;Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A;Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
A;Reference number: A58182; MUID:96149249; PMID:8552191
A;Accession: S68449
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-604 <LIS>
A;Cross-references: UNIPROT:Q13489; EMBL:U45878; NID:g1184315; PIDN:AAC50371.1; PID:g118
C;Function: apoptotic suppressor
A;Description: apoptosis inhibitor
C;Keywords: apoptosis; zinc finger
```

QM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on: January 13, 2005, 15:56:25 ; Search time 650 Seconds
(without alignments)
3058.581 Million cell updates/sec

Sequence: 1 MELTKVAKNGAAATLVMLKN..........TDKCPMCRRTFTNAVRLYFS 346
Title: US-10-041-859-2
Perfect score: 1887
Title: US-10-041-859-2

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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Database : Published_Applications NA:*
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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 1 | 1887 | 100.0 | 3773 | 14 | US-10-041-859-1 | Sequence 1, Appli |
| 2 | 719.5 | 38.1 | 1317 | 16 | US-10-267-502-202 | Sequence 1076, App |
| 3 | 526.5 | 27.9 | 2563 | 16 | US-10-305-720-1076 | Sequence 1076, App |
| 4 | 526.5 | 27.9 | 2563 | 16 | US-10-641-643-894 | Sequence 894, App |
| 5 | 526.5 | 27.9 | 2601 | 15 | US-10-232-286-3 | Sequence 3, Appli |
| 6 | 526.5 | 27.9 | 3076 | 9 | US-09-954-456-1635 | Sequence 1635, Ap |
| 7 | 526.5 | 27.9 | 3076 | 9 | US-09-954-531-16 | Sequence 16, Appli |
| 8 | 526.5 | 27.9 | 3076 | 14 | US-10-197-290-1 | Sequence 157, App |
| 9 | 526.5 | 27.9 | 3076 | 15 | US-10-388-263-157 | Sequence 157, App |
| 10 | 526.5 | 27.9 | 3076 | 17 | US-10-776-827-11 | Sequence 11, Appl |
| 11 | 526.5 | 27.9 | 3164 | 15 | US-10-141-618-5 | Sequence 5, Appli |
| 12 | 526.5 | 27.9 | 3165 | 15 | US-10-269-909-5 | Sequence 564, Appli |
| 13 | 526.5 | 27.9 | 3165 | 15 | US-10-172-118-564 | Sequence 564, App |
| 14 | 526.5 | 27.9 | 3165 | 15 | US-10-366-307-5 | Sequence 5, Appli |
| 15 | 526.5 | 27.9 | 3165 | 16 | US-10-342-887-564 | Sequence 564, App |
| 16 | 526.5 | 27.9 | 5212 | 18 | US-10-825-282-39 | Sequence 39, Appl |
| 17 | 526.5 | 27.9 | 5844 | 10 | US-09-971-392-253 | Sequence 253, Appl |
| 18 | 526.5 | 27.9 | 5857 | 15 | US-10-247-671-18 | Sequence 18, Appl |
| 19 | 525.5 | 27.8 | 2673 | 18 | US-10-482-952-2 | Sequence 2, Appli |
| 20 | 525.5 | 27.8 | 2676 | 9 | US-09-974-592-11 | Sequence 11, Appli |
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| 22 | 525.5 | 27.8 | 6669 | 17 | US-10-636-065-230 | Sequence 230, App |
| 23 | 524.5 | 27.8 | 2676 | 5 | US-09-201-936-5 | Sequence 5, Appli |
| 24 | 524.5 | 27.8 | 2676 | 9 | US-09-201-936-7 | Sequence 7, Appli |
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| 27 | 524.5 | 27.8 | 2916 | 17 | US-10-240-425-1436 | Sequence 1436, Ap |
| 28 | 517.5 | 27.4 | 2450 | 17 | US-10-776-827-31 | Sequence 31, Appl |
| 29 | 517.5 | 27.4 | 2474 | 9 | US-09-201-936-39 | Sequence 39, Appl |
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| 36 | 500.5 | 26.5 | 2589 | 15 | US-10-207-655-199 | Sequence 199, App |
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| 38 | 500.5 | 26.5 | 2589 | 17 | US-10-730-476A-42 | Sequence 42, Appl |
| 39 | 500.5 | 26.5 | 3495 | 17 | US-10-730-476A-43 | Sequence 43, Appl |
| 40 | 500.5 | 26.5 | 3495 | 18 | US-10-482-952-12 | Sequence 12, Appl |
| 41 | 500.5 | 26.5 | 3496 | 14 | US-10-153-668-337 | Sequence 337, App |
| 42 | 500.5 | 26.5 | 3496 | 15 | US-10-172-118-565 | Sequence 565, App |
| 43 | 500.5 | 26.5 | 3496 | 15 | US-10-366-307-3 | Sequence 3, Appli |
| 44 | 500.5 | 26.5 | 3496 | 16 | US-10-342-887-565 | Sequence 565, App |
| 45 | 500.5 | 26.5 | 3532 | 9 | US-09-880-107-3354 | Sequence 3354, Ap |

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/10041859
; Publication No. US20030449796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 1
; LENGTH: 3773
; TYPE: DNA

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;  ORGANISM: Bombyx mori
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (2733)...(3770)
   US-10-041-859-1

US-10-041-859-2 (1-346) x US-10-041-859-1 (1-3773)

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   Score:                   1887.00
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   Best Local Similarity:   100.00%
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   Indels:       0
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Qy     21 AlaAlaArgAspAlaAlaLysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40
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Qy     41 SerThrThrSerThrLeuProSerProSerSerAlaAspLysThrAspAsnHisAla 60
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Qy     61 ThrPheAsnPheLeuProAspMetProAspMetArgGlnGluGluGluLeuArgLeuLysThr 80
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Qy    101 TyrLeuGlyMetTyrArgLeuAlaAsnGlyGlyLeuAlaThrAlaValGlyArgAspGlyCys 120
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Qy    121 ValGlyAlaSerAlaAlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSer 140
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Qy    141 ArgLysGlyMetTyrAlaLeuAlaLeuAlaGlyGlyLysGlyLeuAlaThrAlaValGlyArgGlyArgGluGlyCys 160
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Qy    161 GlyAlaSerAlaLeuAlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSer 180
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Qy    181 ThrGluAlaLeuArgLeuLeuAsnThrPheLysAspTrpProArgMetArgGlnLysPro 200
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Db    746 ACCGAGGCGCTGCGCCTGCTCAACACCTTCAAGGACTGGCCGCGCATGCGCCAAAACCC 805

Qy    201 GluGluLeuLaGluLaGlyPhePheTyrThrGlyIleGlyAspGlyLysThrLysCysPhe 220
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Qy    221 TyrCysGluAspGlyLeuTyrLeuLysAspTrpGluSerAspAspAspValProTrpGluGluGlnHisAla 240
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Qy    261 ValLysSerGluValAlaThrAlaIleSerAlaSerGlyLeuGlyGlnIleAlaLeuThrArgAsnAsp 280
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(second column)

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Qy    321 AlaLysCysAlaLeuSerThrAspLysCysProMetCysArgArgThrPhePheThrAsnAla 340
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Qy    341 ValArgLeuTyrPheSer 346
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; Publication No. US2004001700A1
; GENERAL INFORMATION:
;    APPLICANT: Kim, Jaeseob
;    APPLICANT: Galant, Ron
;    TITLE OF INVENTION: Obesity Linked Genes
;    FILE REFERENCE: LSD-07416
;    CURRENT APPLICATION NUMBER: US/10/267,502
;    CURRENT FILING DATE: 2003-01-27
;    NUMBER OF SEQ ID NOS: 439
;    SOFTWARE: Patentin version 3.2
;    SEQ ID NO 202
;       LENGTH: 1317
;       TYPE: DNA
;    ORGANISM: Drosophila melanogaster
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   Best Local Similarity:   34.92%
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US-10-041-859-2 (1-346) x US-10-267-502-202 (1-1317)

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Qy     88 PheLeuThrProGlnLeuAlaArgAsnGlyPheTyrTyrLeuGlyArgGlyArgGluGlyCysGlyAlaGlu 107
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Db    172 TGGCTGGATAAAACGCCAATTGGCCCAAAССGGCAТACTTCACACACGCCGGCGGACAAA 231

Qy    108 ValCysSerAlaPheCysLysValGlyIleIleMetArgTrpValGluGlyAspAspAspAla 127
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Qy    128 AlaAspHisArgArgTrpLeuAlaProGlnLeuProPheValArgLeuGlnMetTyrAlaAsn 147
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Qy    148 AlaGlyGlyGluValAlaThrAlaValGlyArg---------------- 160
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Qy    161 Gly---------------- 161
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OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: January 13, 2005, 13:51:16 ; Search time 106 Seconds
(without alignments)
2320.122 Million cell updates/sec

Title: US-10-041-859-2
Perfect score: 1887
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Scoring table: BLOSUM62
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Ygapop 10.0 ; Ygapext 0.5
Fgapop 6.0 ; Fgapext 7.0
Delop 6.0 ; Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1311	69.5	1739	4	US-09-502-528-1	Sequence 1, Appli
3	725.5	38.4	1317	4	US-09-586-305A-2	Sequence 2, Appli
4	723.5	38.3	1317	4	US-09-586-305A-1	Sequence 3, Appli
5	723.5	38.3	1317	4	US-09-586-305A-3	Sequence 3, Appli
6	717.5	38.0	1317	4	US-09-586-305A-4	Sequence 4, Appli
7	717.5	38.0	1317	4	US-09-586-305A-5	Sequence 4, Appli
8	715.5	37.9	1317	4	US-09-586-305A-9	Sequence 9, Appli
9	713.5	37.8	1317	4	US-09-586-305A-8	Sequence 10, Appl
10	712.5	37.8	1317	4	US-09-586-305A-10	Sequence 7, Appli
11	712.5	37.8	1317	4	US-09-586-305A-6	Sequence 7, Appli
12	704	37.3	1304	4	US-09-586-305A-8	Sequence 8, Appli
13	526.5	27.9	2563	4	US-09-016-434-1076	Sequence 1076, Ap
14	526.5	27.9	2563	4	US-09-023-655-894	Sequence 894, App
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16	526.5	27.9	2601	5	PCT-US96-12860-3	Sequence 3, Appli
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18	526.5	27.9	3076	4	US-09-814-915A-11	Sequence 11, Appl
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20	525.5	27.8	2676	3	US-08-800-929A-11	Sequence 11, Appl
21	525.5	27.8	2676	3	US-09-617-053A-11	Sequence 11, Appl
22	525.5	27.8	2676	3	US-09-212-971-5	Sequence 5, Appli
23	525.5	27.8	6669	3	US-08-800-929A-5	Sequence 5, Appli
24	525.5	27.8	6669	3	US-09-617-053A-5	Sequence 5, Appli
25	525.5	27.8	6669	3	US-09-672-717-230	Sequence 230, App
26	524.5	27.8	6669	2	US-08-511-485-5	Sequence 5, Appli
27	524.5	27.8	6669	2	US-09-201-936-5	Sequence 5, Appli
28	524.5	27.8	2676	4	US-09-672-717-220	Sequence 220, App
29	524.5	27.8	2676	4	US-09-201-932-5	Sequence 5, Appli
30	524.5	27.8	2916	4	US-09-814-915A-31	Sequence 31, Appl
31	517.5	27.4	2450	4	US-09-201-936-39	Sequence 39, Appl
32	517.5	27.4	2450	4	US-09-201-932-39	Sequence 39, Appl
33	517.5	27.4	2474	4	US-09-201-356-39	Sequence 39, Appl
34	517.5	27.4	2474	4	US-09-672-717-226	Sequence 226, App
35	517.5	27.4	2580	2	US-08-511-485-7	Sequence 7, Appl
36	507.5	26.9	2580	4	US-09-011-356-7	Sequence 7, Appli
37	507.5	26.9	2580	4	US-09-672-717-222	Sequence 222, App
38	507.5	26.9	2580	4	US-09-201-932-7	Sequence 7, Appli
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41	500.5	26.5	2589	5	PCT-US96-12860-1	Sequence 1, Appli
42	500.5	26.5	3532	2	US-09-205-204-1	Sequence 1, Appli
43	500.5	26.5	3532	2	US-09-212-971-7	Sequence 7, Appli
44	500.5	26.5	3732	3	US-08-800-929A-7	Sequence 7, Appli
45	500.5	26.5	3732	3	US-08-800-929A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-502-528-2
; Sequence 2, Application US/09502528
; Patent No. 6570069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibitors of Apoptosis
; FILE REFERENCE: 02307O-1120000US
; CURRENT APPLICATION NUMBER: US/09/502,528
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 2
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Spodoptera frugiperda
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1134)
; OTHER INFORMATION: (ORF) only
; OTHER INFORMATION: SfIAP nucleotide sequence, open reading frame
; OTHER INFORMATION: (SfIAP)
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
US-09-502-528-2

Alignment Scores:
Pred. No.:   2.38e-132   Length: 1134
Score: 1311.00   Matches: 248
Percent Similarity: 79.28%   Conservative: 39
Best Local Similarity: 68.51%   Mismatches: 57
Query Match: 69.48%   Indels: 18
DB: Gaps: 7

US-10-041-859-2 (1-346) x US-09-502-528-2 (1-1134)

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Qy      1 MetGluLeuThrLysValAlaLysAsnGlyAlaAlaAlaThrLeuValMetLeuLysAsn 20
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Db     52 ATGGATAATTACCAAAAGTGGCATCCAAATGGCTCCTCCTCAACATTAACCGTATTCAAGAGC 111

Qy     21 ---AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeu------SerSer 37
          ||||:||||||||||||||||||||||||||||||||           |||
Db    112 GGATCGGCTTGAGGCGTAAAAATTCGACCT---CTCCGCGCCACTAAGCTGCCGACCCCAAGT 168

Qy     38 CysGluSerSerThrThrSerThrLeuProSerProSerSer------------------- 51
          |||||||||||||||||||||||:||:
Db    169 TACGACTCCAACGCCGCGGCGTCTCCATCTTTGTCTCCATCCACGCCTTGCTCTTCATCTTCT 228

Qy     52 ---SerAlaAspLysThrAspAsnHisAspThrPheAsnPheLeuProAspMetProAsp 70
          |||:|||||||||::||||||||:||||||||||||||||::|||
Db    229 TTCTCCATTGATAAAACCGACAACCACACCTTTCGGCTTCAGTGCCGACACAGTTGAT 288

Qy     71 MetArgArgGluGluGluGluArgLeuLysThrPheAspGlnTrpProValThrProLeuThr 90
          :::||||||||||||||::||:::
Db    289 ATGAGAAAAGAGGATGAACGTACCAAAACATTTGAAAAAATGGCCCGTAAGTTTGTTGTGTAG 348

Qy     91 ProGluGlnLeuAlaArgAlaAsnGlyPheTyrTyrLeuGlyArgGlyAspGluValCysCys 110
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Db    349 GGAGAGCAACTTGCTCGAAATGGATTTTACTACCTCGGCCGTGGAGATGAAGCCCGGTTGC 408

Qy    111 AlaPheCysLysValGluIleMetArgTrpValGluGlyAspAspProAlaAlaAspHis 130
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Db    409 GCTTTCTGTAAAGTGGAGATTATGAGGTGGGTGGAGGGCGATGACCCTGCGAGGACCAT 468

Qy    131 ArgArgTrpAlaProGlnCysProPheValArgLysGlnMetTyrAlaAsnAlaGlyGly 150
          :::||||||||||||||||||||||||||||||||||||:::
Db    469 CACGGTTGGGCGCCACAGTGCCCATTTGTGCGCAAA---TTGAACGGTACTGCAGCACA 525

Qy    151 GlyAlaThrAlaValGlyArgAspGlyCysGlyAlaSerAlaAla------ThrGln 167
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Db    526 GACACAGGGTAGTTCGGCCAGGACGAGTGTGGTGCCCGGCGCTCCCTCCGTACTTCT 585

Qy    168 ProProArgMetProGlyProValHisAlaArgTyrSerThrGluAlaArgLeuAla 187
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Db    586 CCCCGCCGGTATGCCCGGTCCCGTTGCACCCACCGATTATGCATCTCGAAGCCGACGACTACGC 645

Qy    188 ThrPheLysValAspTrpProArgArgMetArgGlnLysProGluGluLeuAlaGluAlaGly 207
          ::||||||||||||||||||||||||||||||::||
Db    646 AGTTTTAAAGACTGGCCACGATGCGACCAAAAACCTGAAGAACTTGCCGAGGCCTGGC 705

Qy    208 PhePheTyrThrGlyIleGlyAspLysThrLysCysPheTyrCysAspGlyGlyLeuLys 227
          ||||||||||||||||||||||:||||||||||||||||||||||||||::
Db    706 TTTTTTTTACACTGGTCAGGGAGACAAAACCAAGTGTTTTTTATTGCGATGGGTGGATTAAAA 765

Qy    228 AspTrpGluSerAspAspValProThrGlnHisHisAlaArgTrpPheAspArgGlyCysAla 247
          :::||||||||||||||||||||||||||::||
Db    766 GATTGGGAGAACCATGACGTACCCTGGGAACACGCAAGGTGGTTTGACCCGTTGCGCC 825

Qy    248 TyrValGlnLeuValLysGlyTyrIleGlnLysValLysSerGluAlaThrAla 267
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Db    826 TACGTGCAATTGGTGAAGGGTCGAGAATACGTTCAAAAGGTGAATTCTGAAGTTGTGTAG 885

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Db    886 GTATCCCGCGTCAGAAGAGGAGCAGTGTAGACCCCACGGACTGCGCGACCCAAGCCCG 945

Qy    285 ValAlaGlnLeuGlyLysHisSerLeuAspSerGlyIleCysLysIleCysTyrSer 304
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Qy    305 GluGlyArgAsnValCysPheValAlaCysSerAlaValCysSerAla 324
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Db   1006 GAAGAGCGTAACCGTGTGTCCTTCGTGCCGTGGCCTGGCCAAGTGCCG 1065

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Db   1066 CTGGGCGCCGACAAGTGCCCCATGTGCCGCAGGACGTTTCAAAATGCAGTGCGGGTTATAT 1125
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Qy    345 PheSer 346
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Db   1126 TTCTCG 1131
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RESULT 2

US-09-502-528-1

; Sequence 1, Application US/09502528
; Patent No. 6570069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibitors of Apoptosis
; FILE REFERENCE: 023070-112000US
; CURRENT APPLICATION NUMBER: US/09/502,528
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 1
; LENGTH: 1739
; TYPE: DNA
; ORGANISM: Spodoptera frugiperda
; FEATURE:
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SfIAP) nucleotide sequence including 5' and 3'
; OTHER INFORMATION: untranslated regions, full length SfIAP cDNA
; NAME/KEY: CDS
; LOCATION: (229)..(1362)
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
US-09-502-528-1

Alignment Scores:
Pred. No.:
Score: 1311.00
Percent Similarity: 79.28%
Best Local Similarity: 68.51%
Query Match: 69.48%
DB:

US-10-041-859-2 (1-346) x US-09-502-528-1 (1-1739)

Length:	1739	
Matches:	248	
Conservative:	39	
Mismatches:	57	
Indels:	18	
Gaps:	7	

```
Qy      1 MetGluLeuThrLysValAlaLysAsnGlyAlaAlaAlaThrLeuValMetLeuLysAsn 20
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Db    280 ATGGATAATTACCAAAAGTGGCATCCAAATGGCTCCTCCTCAACATTAACCGTATTCAAGAGC 339

Qy     21 ---AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeu------SerSer 37
          ||||:||||||||||||||||||||||||||||||||           |||
Db    340 GGATCGGCTTGAGGCGTAAAAATTCGACCT---CTCCGCGCCACTAAGCTGCCGACCCCAAGT 396

Qy     38 CysGluSerSerThrThrSerThrLeuProSerProSerSer------------------- 51
          |||||||||||||||||||||||:||:
Db    397 TACGACTCCAACGCCGCGGCGTCTCCATCTTTGTCTCCATCCACGCCTTGCTCTTCATCTTCT 456

Qy     52 ---SerAlaAspLysThrAspAsnHisAspThrPheAsnPheLeuProAspMetProAsp 70
          |||:|||||||||::||||||||:||||||||||||||||::|||
Db    457 TTCTCCATTGATAAAACCGACAACCACACCTTTCGGCTTCAGTGCCGACACAGTTGAT 516

Qy     71 MetArgArgGluGluGluGluArgLeuLysThrPheAspGlnTrpProValThrProLeuThr 90
          :::||||||||||||||::||:::
Db    517 ATGAGAAAAGAGGATGAACGTACCAAAACATTTGAAAAAATGGCCCGTAAGTTTGTTGTGTAG 576

Qy     91 ProGluGlnLeuAlaArgAlaAsnGlyPheTyrTyrLeuGlyArgGlyAspGluValCysCys 110
          :::||||||||||||||||||||||||||||||||||||||||||:::
Db    577 GGAGAGCAACTTGCTCGAAATGGATTTTACTACCTCGGCCGTGGAGATGAAGCCCGGTTGC 636

Qy    111 AlaPheCysLysValGluIleMetArgTrpValGluGlyAspAspProAlaAlaAspHis 130
          |||:||:|||||||||||||||||||:||||||||||||||||
Db    637 GCTTTCTGTAAAGTGGAGATTATGAGGTGGGTGGAGGGCGATGACCCTGCGAGGACCAT 696

Qy    131 ArgArgTrpAlaProGlnCysProPheValArgLysGlnMetTyrAlaAsnAlaGlyGly 150
          :::||||||||||||||||||||||||||||||||||||:::
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 13, 2005, 13:35:09 ; Search time 569 Seconds
                       (without alignments)
                       3192.091 Million cell updates/sec

Title: 1887
Perfect score: 1887
Sequence: 1 MELTKVAXNGAAATLVWLKN..........TDKCPMCRRTFTNAVRLYFS 346

Searched: US-10-041-859-2

Scoring table: BLOSUM62
                       Xgapop   10.0 :   Xgapext   0.5
                       Ygapop   10.0 :   Ygapext   0.5
                       Fgapop   6.0 :   Fgapext   7.0
                       Delop   6.0 :   Delext   7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model1 -DEV=xlh
 1:   geneseqn1980s:*
 2:   geneseqn1990s:*
 3:   geneseqn2000s:*
 4:   geneseqn2001as:*
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 6:   geneseqn2002as:*
 7:   geneseqn2002bs:*
 8:   geneseqn2003as:*
 9:   geneseqn2003bs:*
10:   geneseqn2003cs:*
11:   geneseqn2003ds:*
12:   geneseqn2004s:*

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-Db=N_Geneseq_23Sep04 -OFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPExt=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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Database :   N_Geneseq_23Sep04:*

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	1887	100.0	3773	6	ABQ78228	Abq78228 Nucleotid
2	1311	69.5	1739	5	AAD14419	Aad14419 Fall army
3	787	41.7	50000	6	ABL55643	Abl55643 AmEPV gen
4	748	39.6	794	6	ABL55635	Abl55635 AmEPV bac
5	721.5	38.2	1317	5	AAC84521	Aac84521 Drosophil
6	719.5	38.1	1317	5	AAC84520	Aac84520 Drosophil

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

RESULT 1
ABQ78228
ID   ABQ78228 standard; cDNA; 3773 BP.
XX
AC   ABQ78228;
XX
DT   22-OCT-2002   (first entry)
XX
DE   Nucleotide sequence of inhibitor of apoptosis protein BmIAP.
XX
KW   Inhibitor of apoptosis protein; IAP; BmIAP; silkworm; apoptosis; insect;
KW   Spodoptera frugiperda; insult-resistant plant; caspase; gene; ss.
XX
OS   Bombyx mori.
XX
FH   Key   Location/Qualifiers
FT   CDS   2733..3773
FT   /*tag=   a
FT   /product= "inhibitor of apoptosis protein BmIAP"
XX
PN   WO200253586-A2.
XX
PD   11-JUL-2002.
XX
PF   07-JAN-2002; 2002WO-US000314.
XX
PR   08-JAN-2001; 2001US-0260478P.
XX
PA   (BURN-) BURNHAM INST.

ALIGNMENTS

(the table of scores and IDs running down the page:)

7	719.5	38.1	1317	5	AAC84522	Aac84522 Drosophil
8	719.5	38.1	1317	12	ADO07876	Ado07876 Fly polyn
9	719.5	38.1	1858	6	ABL21061	Abl21061 Drosophil
10	719.5	38.1	2013	4	ABL10083	Abl10083 Drosophil
11	719.5	38.1	10432	4	ABL10082	Abl10082 Drosophil
12	719.5	38.1	14250	4	ABL21060	Abl21060 Drosophil
13	713.5	37.8	1317	5	AAC84523	Aac84523 Drosophil
14	713.5	37.8	1317	5	AAC84524	Aac84524 Drosophil
15	711.5	37.7	1317	5	AAC84528	Aac84528 Drosophil
16	709.5	37.6	1317	5	AAC84529	Aac84529 Drosophil
17	708.5	37.5	1317	5	AAC84525	Aac84525 Drosophil
18	708.5	37.5	1304	5	AAC84526	Aac84526 Drosophil
19	700	37.1	131680	5	AAC84527	Aac84527 Drosophil
20	546.5	29.0	131680	10	ADF29092	Adf29092 Agrotis s
21	526.5	27.9	2563	10	ADB80989	Adb80989 RING-SH c
22	526.5	27.9	2563	10	ACA56478	Aca56478 Human sig
23	526.5	27.9	2563	11	ADI31568	Adi31568 Human cDN
24	526.5	27.9	2563	12	ADI56274	Adi56274 Human pol
25	526.5	27.9	2601	2	AAT61591	Aat61591 Human C-I
26	526.5	27.9	3076	2	AAT72712	Aat72712 Human inh
27	526.5	27.9	3076	2	AAZ41005	Aaz41005 Human cel
28	526.5	27.9	3076	2	AAZ22096	Aaz22096 Human cel
29	526.5	27.9	3076	6	ABL62746	Abl62746 Breast ca
30	526.5	27.9	3076	6	ABL66325	Abl66325 Lung canc
31	526.5	27.9	3076	8	ABX10968	Abx10968 cDNA enco
32	526.5	27.9	3076	10	AAD60472	Aad60472 Human cel
33	526.5	27.9	3164	10	ABV75363	Abv75363 Human CIA
34	526.5	27.9	3164	12	ADG87134	Adg87134 Human CIA
35	526.5	27.9	3165	12	ADH74642	Adh74642 cDNA enco
36	526.5	27.9	3076	2	ABX10333	Abx10333 DNA encod
37	526.5	27.9	5844	10	ADB47553	Adb47553 Human cDN
38	526.5	27.9	5857	10	ADE25614	Ade25614 Human cDN
39	526.5	27.8	2673	6	ABZ58100	Abz58100 Mouse inh
40	525.5	27.8	2676	2	AAV55042	Aav55042 Murine HI
41	525.5	27.8	6669	6	AAV55039	Aav55039 Human HIA
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43	524.5	27.8	3164	12	AAT70837	Aat70837 Human apo
44	524.5	27.8	2676	2	ABK93870	Abk93870 Human cDN
45	524.5	27.8	2916	12	ADF45449	Adf45449 Human vas

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PI
DR   WPI; 2002-590628/63.
DR   P-PSDB; ABB78046.
XX
PT   Novel recombinant polypeptide, inhibitor of apoptosis protein family
PT   member BmIAP from silkworm Bombyx mori BmN cells, useful for inhibiting
PT   apoptosis and identifying an agent that modulates activity of
PT   polypeptide.
XX
```

Maeda S, Huang Q, Reed JC, Deveraux QL;

```
PS   Claim 8; Page 29-30; 62pp; English.
XX
CC   The present scone encodes a polypeptide which is an inhibitor of
CC   apoptosis protein (IAP) family member, and designated BmIAP. BmIAP is
CC   derived from silkworm Bombyx mori BmN cells. The BmIAP polypeptide
CC   contains two baculoviral IAP repeat (BIR) domains, followed by a RING
CC   domain. BmIAP polypeptides and polynucleotides are useful for inhibiting
CC   apoptosis in insect cells, especially Spodoptera frugiperda or Bombyx
CC   mori cells, and mammalian cells, and plant cells. They are also useful
CC   for generating a biotic or abiotic insult-resistant plant. BmIAP is also
CC   useful for inhibiting caspases
XX
SQ   Sequence 3773 BP; 1108 A; 785 C; 866 G; 1014 T; 0 U; 0 Other;
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US-10-041-859-2 (1-346) x ABQ78228 (1-3773)

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Alignment Scores:
Pred. No.:
Pred.:
Score:                 1887.00       Length:        3773
Percent Similarity:    100.00%       Matches:       346
Best Local Similarity: 100.00%       Conservative:  0
Query Match:           100.00%       Mismatches:    0
                                     Indels:        0
                                     Gaps:          0
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Qy    1 MetGluLeuThrLysValAlaLysAsnGlyAlaAlaAlaThrLeuValMetLeuLysAsn 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  206 ATGGAGTTGACGAAAGTTGCTAAAAATGGAGCGCCGCCACGTTGGTGATGTTAAAAAAT 265

Qy   21 AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  266 GCGCGCGGGATGCAAAAATGCGACCTTTCATTGGTCCGCTCCTCATGTTATCCTCGTGTGAGTCT 325

Qy   41 SerThrThrSerThrLeuProSerProSerSerAlaAspLysThrAspAsnHisAsp 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  326 TCAACGACANTCCACACTCCCGTCACCTTCGTCGTCAGCGTGATAAAACGGATAATCACGAC 385

Qy   61 ThrPheAsnPheLeuProAspMetProAspMetArgArgGluGluGluArgLeuLysThr 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  386 ACANTTCAACTTCCTTCCCGATATGCCCGACATGCGTCGTCTGAAGAGGAACGTCTGAAAACA 445

Qy   81 PheAspGlnTrpProValThrProLeuThrProGlnLeuIleLeuAlaArgAsnGlyPheTyr 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  446 TTTGATCACGTGGCCCGTTACGTTTTGACGCCGGAACAATTGGCCCGGAACGGATTCTAC 505

Qy  101 TyrLeuGlyArgGlyAspValValCysSerAlaPheCysLysSerValGluIleMetArgTrp 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  506 TACTTCGGTCGCGGCGACGAAGTGGTGTGCTCGGCTTTCTGTAAGGTAGAAATTATGAGGTGG 565

Qy  121 ValGluGlyAspProArgLeuAspProArgGlnCysProPheVal 140
          |||||||||||||||||||||||||||||||||||||||||||
Db  566 GTCGAAGGCGACGATCCTCGCCGGCGATCATCGACAGTGGGCCGCCCCCAGTGTCCCTTTGTA 625

Qy  141 ArgGlyLysGlnMetTyrAlaAsnAlaGlyGlyLysAlaThrAlaValGlyArgAspGluCys 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  626 CGAAAACAAATGTATGCCAACGCTGGGGGAGAGGACGACCCGCTTGCGGTTAGAGACGAATGT 685

Qy  161 GlyAlaSerAlaLysThrGlnLeuProProArgMetProGlyProValHisAlaAlaArgTyrSer 180
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Db  686 GGGGCCAGTGCGGGCCACGCAGCCTCCCCCGATCATGCCCGGCCCGTGCACGGCGTACTCC 745

Qy  181 ThrGluAlaIleAlaAlaArgLeuAlaThrPheLysAspTrpProAspArgArgMetGlnLysPro 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  746 ACCGAGGCCGCGGCGCTCGCCACCTTCAAGGACTGGCCGGACCGTATGCGCCAAAAACCC 805

Qy  201 GluGluLeuAlaGluAlaGlyPhePheTyrThrGlyGlnGlyAspLysThrLysCysPhe 220
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Db  806 GAGGAACTGGCAGAAGCAGGGCCGTTCTTCTATACAGGCCAAGGTGACAAAACGAAATGCTTC 865

Qy  221 TyrCysAspGlyGlyLeuLysAspTrpGluSerAspAspValProTrpGluGlnHisAla 240
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Qy  241 ArgTrpPheAspAlaArgCysAlaTyrValGlnLeuValGlyTyrArgAspTyrIleGlnLys 260
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Db 1166 GCCAAGTGCGCGCTGTCGACGGACAAGTGCCCGATGTGTCGCAGGACGTTCACGAATGCG 1225

Qy  341 ValArgLeuTyrPheSer 346
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Db 1226 GTGCGGCTCTACTTCTCG 1243
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RESULT 2
AAD14419
ID   AAD14419 standard; cDNA; 1739 BP.
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AC   AAD14419;
XX
DT   01-NOV-2001 (first entry)
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DE   Fall armyworm inhibitor of apoptosis (IAP) cDNA.
XX
KW   Fall armyworm; inhibitor of apoptosis; IAP; transgenic plant;
KW   apoptosis inhibitor; therapy; acquired immune deficiency syndrome; AIDS;
KW   neurodegenerative disease; Alzheimer's disease; aplastic anaemia;
KW   Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;
KW   myelodysplastic syndrome; toxin-induced liver disease; ischaemic injury;
KW   myocardial infarction; stroke; reperfusion injury; cancer; nootropic;
KW   autoimmune disorder; lupus erythematosus; multiple sclerosis; vasotropic;
KW   insecticide; viral infection; anti-HIV; human immunodeficiency virus;
KW   neuroprotective; antianaemic; cardiant; cerebroprotective; vulnerary;
KW   cytostatic; immunosuppressive; virucide; antialcoholic; ss.
XX
OS   Spodoptera frugiperda.
XX
FH   Key            Location/Qualifiers
FT   CDS            229..1362
FT                  /tag= a
FT                  /product= "Inhibitor of apoptosis protein"
FT                  /note= "CDS is referred as SEQ ID NO 2 in the
FT                  specification"
XX
PN   WO200159108-A2.
XX
PD   16-AUG-2001.
XX
PF   07-FEB-2001; 2001WO-US004071.
XX
PR   10-FEB-2000; 2000US-00502528.
XX
PA   (REGC ) UNIV CALIFORNIA.
PA   (MAED/) MAEDA H.
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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:　　　　January 6, 2005, 19:29:14 ; Search time 148 Seconds
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Title:　　　　　　US-10-041-859-2
Perfect score:　1887
Sequence:　　　　1 MELTKVAKNGAAATLVMLKN...........TDKCPMCRRTFTNAVRLYFS 346

Scoring table:　BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:　　　　1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters:　　1603904

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :　　　Published_Applications_AA:*
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　　6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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　13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
　14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
　15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
　16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
　17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	1887	100.0	346	14	US-10-041-859-2	Sequence 2, Appli
2	966	51.2	275	9	US-09-201-936-12	Sequence 12, Appl
3	966	51.2	275	14	US-10-323-643-9	Sequence 9, Appli
4	966	51.2	275	16	US-10-600-272-12	Sequence 12, Appl
5	932.5	49.4	172	14	US-10-041-859-8	Sequence 8, Appli
6	862	45.7	268	14	US-10-323-643-10	Sequence 10, Appl
7	846.5	44.9	172	14	US-10-041-859-9	Sequence 9, Appli
8	831.5	44.1	172	14	US-10-041-859-9	Sequence 9, Appl
9	759.5	40.2	172	14	US-10-041-859-11	Sequence 11, Appl
10	719.5	38.1	438	15	US-10-267-502-419	Sequence 419, App
11	696.5	36.9	172	14	US-10-041-859-12	Sequence 12, Appl
12	554.5	29.4	172	14	US-10-041-859-13	Sequence 13, Appl
13	526.5	27.9	604	14	US-10-232-286-4	Sequence 4, Appli
14	526.5	27.9	604	14	US-10-141-618-6	Sequence 6, Appli
15	526.5	27.9	604	14	US-10-366-307-6	Sequence 6, Appli
16	526.5	27.9	604	16	US-10-730-476A-79	Sequence 79, Appl
17	526.5	27.9	604	17	US-10-825-282-40	Sequence 40, Appl
18	525.5	27.8	600	17	US-09-974-592-12	Sequence 12, Appl
19	525.5	27.8	600	17	US-10-482-952-1	Sequence 1, Appli
20	524.5	27.8	604	9	US-09-974-592-6	Sequence 6, Appli
21	524.5	27.8	604	16	US-09-201-936-6	Sequence 6, Appli
22	524.5	27.8	604	16	US-10-636-065-221	Sequence 221, App
23	524.5	27.8	604	16	US-10-600-272-6	Sequence 6, Appli
24	517.5	27.4	602	16	US-09-201-936-40	Sequence 40, Appl
25	517.5	27.4	602	16	US-10-636-065-227	Sequence 227, App
26	517.5	27.4	602	16	US-10-600-272-40	Sequence 40, Appl
27	507.5	26.9	618	9	US-09-974-592-8	Sequence 8, Appli
28	507.5	26.9	618	16	US-09-201-936-8	Sequence 8, Appli
29	507.5	26.9	618	16	US-10-636-065-223	Sequence 223, App
30	507.5	26.9	618	16	US-10-600-272-8	Sequence 8, Appli
31	500.5	26.5	498	16	US-10-153-668-338	Sequence 338, Appl
32	500.5	26.5	498	16	US-10-207-655-200	Sequence 200, App
33	500.5	26.5	618	14	US-10-232-286-2	Sequence 2, Appli
34	500.5	26.5	618	14	US-10-366-307-4	Sequence 4, Appli
35	500.5	26.5	618	15	US-10-260-708-63	Sequence 63, Appli
36	500.5	26.5	618	15	US-10-361-270-3	Sequence 3, Appli
37	500.5	26.5	618	17	US-10-482-952-11	Sequence 11, Appl
38	500.5	26.5	618	14	US-10-730-476A-78	Sequence 78, Appl
39	499.5	26.5	499	16	US-10-366-307-2	Sequence 2, Appli
40	500.5	26.5	618	9	US-09-974-592-4	Sequence 4, Appli
41	499.5	26.5	497	14	US-09-201-936-4	Sequence 4, Appli
42	497.5	26.4	497	9	US-09-974-592-4	Sequence 4, Appli
43	497.5	26.4	497	16	US-10-636-065-219	Sequence 219, App
44	497.5	26.4	497	16	US-10-600-272-4	Sequence 4, Appli
45	497.5	26.4	497	16	US-10-041-859-2	

ALIGNMENTS

RESULT 1
US-10-041-859-2
; Sequence 2, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 08710Z/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Bombyx mori
US-10-041-859-2

Query Match　　　100.0%;　Score 1887;　DB 14;　Length 346;
Best Local Similarity　100.0%;　Pred. No. 1.7e-169;
Matches　346;　Conservative　0;　Mismatches　0;　Indels　0;　Gaps　0;

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Qy　61 TFNFLPDMPDMRREEERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCCAFCKVEIMRW 120
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RESULT 3

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Db  181  TEAARLATFKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKDWESDDVPWEQHA  240

Qy  241  RWFDRCAYVQLVKGRDYIQKVKSEATAISASEBEQAATNDSTKNVAQEGEKHLDDSKICK  300
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Db  241  RWFDRCAYVQLVKGRDYIQKVKSEATAISASEBEQAATNDSTKNVAQEGEKHLDDSKICK  300

Qy  301  ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS  346
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Db  301  ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS  346
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RESULT 2
US-09-201-936-12

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; Sequence 12, Application US/09201936
; Publication No. US20020179946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 0789I/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Cydia pomonella
US-09-201-936-12
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Best Local Similarity   59.2%; Pred. No.1.3e-82;
Matches 171; Conservative 39; Mismatches 55; Indels 24; Gaps 3;

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Qy  128  ADHRRWAPQCFVRKQMYANAGGEATAVGRDECGASAATQ------PPRMPGPVHARYS  180
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Qy  181  TEAARLATFKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKDWESDDVPWEQHA  240
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Db  107  HEAARVKSFHNWPRCMKQRPEQMADAGFFYTGYGDNTKCFYCDGGLKDWEPEDVPWEQHV  166

Qy  241  RWFDRCAYVQLVKGRDYIQKVKSEATAI---SASEBEQAATNDSTKNVAQEGEKHLDDSK  297
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Db  167  RWFDRCAYVQLVKGRDYVQKVITEACVLPGENTTVSTAAPVSEPIPETKIEKEPQVEDSK  226

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US-10-323-643-9

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; Sequence 9, Application US/10323643
; Publication No. US20030108552A1
; GENERAL INFORMATION:
; APPLICANT: He, et al.
; TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
; FILE REFERENCE: PF165PID1
; CURRENT APPLICATION NUMBER: US/10/323,643
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 08/464,588
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US95/05922
; PRIOR FILING DATE: 1995-05-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Cydia pomonella granulovirus
US-10-323-643-9
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Query Match   51.2%; Score 966; DB 14; Length 275;
Best Local Similarity   59.2%; Pred. No.1.3e-82;
Matches 171; Conservative 39; Mismatches 55; Indels 24; Gaps 3;

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Qy  128  ADHRRWAPQCFVRKQMYANAGGEATAVGRDECGASAATQ------PPRMPGPVHARYS  180
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Db  167  RWFDRCAYVQLVKGRDYVQKVITEACVLPGENTTVSTAAPVSEPIPETKIEKEPQVEDSK  226

Qy  298  ICKICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS  346
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RESULT 4
US-10-600-272-12

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; Sequence 12, Application US/10600272
; Publication No. US20040015732A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 0789I/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 275
; TYPE: PRT
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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: January 6, 2005, 18:43:17 ; Search time 30 Seconds
                                            (without alignments)
                                            764.868 Million cell updates/sec

Title: US-10-041-859-2
Perfect score: 1887
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Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents AA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1311	69.5	377	4	US-09-502-528-3	Sequence 3, Appli
2	966	51.2	275	3	US-08-511-485-12	Sequence 12, Appl
3	966	51.2	275	3	US-08-836-134-21	Sequence 21, Appl
4	966	51.2	275	4	US-09-493-784-21	Sequence 21, App
5	966	51.2	275	4	US-09-201-936-12	Sequence 12, Appl
6	966	51.2	275	4	US-09-011-356-12	Sequence 12, Appl
7	966	51.2	275	3	US-09-201-932-12	Sequence 12, Appl
8	862	45.7	268	3	US-08-836-134-22	Sequence 22, Appl
9	862	45.7	268	4	US-09-493-784-22	Sequence 22, Appl
10	725.5	38.4	438	4	US-09-586-305A-12	Sequence 12, Appl
11	723.5	38.3	438	4	US-09-586-305A-11	Sequence 11, Appl
12	723.5	38.3	438	4	US-09-586-305A-13	Sequence 13, Appl
13	717.5	38.0	438	4	US-09-586-305A-14	Sequence 14, Appl
14	717.5	38.0	438	4	US-09-586-305A-15	Sequence 15, Appl
15	715.5	37.9	438	4	US-09-586-305A-19	Sequence 19, Appl
16	713.5	37.8	438	4	US-09-586-305A-20	Sequence 20, Appl
17	712.5	37.8	438	4	US-09-586-305A-16	Sequence 16, Appl
18	712.5	37.8	438	4	US-09-586-305A-17	Sequence 17, Appl
19	531.5	28.2	438	4	US-09-586-305A-18	Sequence 18, Appl
20	526.5	27.9	604	3	US-08-569-749-4	Sequence 4, Appli
21	526.5	27.9	604	5	PCT-US96-12860-4	Sequence 4, Appli
22	525.5	27.8	600	3	US-09-212-971-12	Sequence 12, Appl
23	525.5	27.8	600	3	US-08-800-929A-12	Sequence 12, Appl
24	525.5	27.8	600	3	US-09-617-053A-12	Sequence 12, Appl
25	524.5	27.8	600	2	US-08-511-485-6	Sequence 6, Appli
26	524.5	27.8	604	3	US-09-212-971-6	Sequence 6, Appli
27	524.5	27.8	604	3	US-08-800-929A-6	Sequence 6, Appli
28	524.5	27.8	604	3	US-09-617-053A-6	Sequence 6, Appli
29	524.5	27.8	604	4	US-09-201-936-6	Sequence 6, Appli
30	524.5	27.8	604	4	US-09-011-356-6	Sequence 6, Appl
31	524.5	27.8	604	4	US-09-672-717-221	Sequence 221, App
32	517.5	27.4	602	4	US-09-201-936-40	Sequence 40, Appl
33	517.5	27.4	602	4	US-09-011-356-40	Sequence 40, Appl
34	517.5	27.4	602	4	US-09-201-932-12	Sequence 12, Appl
35	517.5	27.4	602	4	US-09-672-717-227	Sequence 227, App
36	507.5	26.9	602	2	US-09-201-932-40	Sequence 40, Appl
37	507.5	26.9	618	2	US-08-511-485-8	Sequence 8, Appli
38	507.5	26.9	618	3	US-09-212-971-8	Sequence 8, Appli
39	507.5	26.9	618	3	US-08-800-929A-8	Sequence 8, Appli
40	507.5	26.9	618	3	US-09-617-053A-8	Sequence 8, Appli
41	507.5	26.9	618	4	US-09-201-936-8	Sequence 8, Appli
42	507.5	26.9	618	4	US-09-011-356-8	Sequence 8, Appli
43	507.5	26.9	618	4	US-09-672-717-223	Sequence 223, App
44	507.5	26.9	618	4	US-09-201-932-8	Sequence 8, Appli
45	501	26.6	497	4	US-08-657-759-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-502-528-3

; Sequence 3, Application US/09502528
; Patent No. 6570069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibitors of Apoptosis
; FILE REFERENCE: 023070-11200US
; CURRENT APPLICATION NUMBER: US/09/502,528
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 377
;   TYPE: PRT
;   ORGANISM: Spodoptera frugiperda
;   FEATURE:
;   OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
;   OTHER INFORMATION: (SfIAP)
US-09-502-528-3

Query Match   69.5%; Score 1311; DB 4; Length 377;
Best Local Similarity   68.5%; Pred. No. 1.2e-128;
Matches 248; Conservative 39; Mismatches 57; Indels 18; Gaps 7;

Qy   1 MELTKVAKNGAAATLVMLKN-ARDAKQRPFIGPLML--SSCESSTTSTLPSFSS------ 51
            ::||||||||||||||||||| |:::|||:||.||| :|:|||||:||:|||
Db   18 MDITKVASNGSSSSTLTLPKSGSLLEAKIRP-LAPLMLPFPSYSDSNAGSFSPSLSPSTPCSSSS 76

Qy   52 -SADKTDNHDTFNFLPDMPDMRREEERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCC 110
            |:||:|||:|:|:||||||||:|||||::|:||||:|:||||:||||||:|||:|||
Db   77 FSIDKTDNHDTFGFSADTVDMRKEDERMKTFEKWPVSFLSGEQLARNGFYYLGRRDEARC 136

Qy   111 AFCKVEIMRWVEGDDPAADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAA---TQ 167
            ||||||||||||||||:.|:|||||||||||||.|:.|:||:|:||||:|||:| |
Db   137 AFCKVEIMRWVEGDDPAKDHQRWAPQCPFVRK-LNGTAAADTGSSGQDECGARAAPSGTS 195

Qy   168 PPRMPGPVHARYSTEAARLATFKDWPRRMRMRQKPEELAEAGFPYTGQGDKTKCFYCDGGLK 227
            |||:||||:|||:::||||:|:||||:|:|:||||||||||||||||||||:|||||||||
Db   196 PPRMAGPVHPRYASEAARLRSFKDWPRCMRQKPEELAEAGFPYTGQGDKTKCFYCDGGLK 255

Qy   228 DWESDDVPWEQHARWFDRCAYQLVKGRDYIQKVKSRATAIASASEEEQ---AATNDSTKN 284
            ||:.|||||||||||||||||||:|||||:|||:|.:|:|:|||||||: ||:||:||
Db   256 DWENHDVPWEQHARWFDRCAYVQLVKGREYVQKVISEACEVSASAEARDVAPARTAEPSP 315

Qy   285 VAQEGEKHLDDSKICKICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLY 344
            |:| |.||||||||||||||||||||||||||||||||||||||||||||
Db   316 [continues]

```
Db   316 PAEAPENSVDDSKLCKICYAEERNVCFVPCGHVVACAKCALAADKCPMCRRTFQNAVRLY 375

Qy   345 FS 346
         |  |
Db   376 FS 377
```

RESULT 2
US-08-511-485-12
; Sequence 12, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Ikeda, John-e
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-12

Query Match   51.2%; Score 966; DB 2; Length 275;
Best Local Similarity   59.2%; Pred. No. 1e-92;
Matches   171; Conservative 39; Mismatches 55; Indels 24; Gaps 3;

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Qy    68 MPDMREEERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCCAFCKVEIMRWVEGDDPA 127
         |:|||||||||||||:||||:||:|||||||||||||||||||||||||:||||||||||
Db     1 MSDLRLEEVRLNTFEKWPVSFLSPETMAKNGFYYLGRSDEVRCAFCKVEIMRWKEGEDDA  60

Qy   128 ADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAATQ------PPRMPGVHARYS 180
         |||:||:|||||:|:                :|||||:||:|||||||:|:
Db    61 ADHKKWAPQCPFVK----------GIDVCGSIVTLNNIQNTTHDTIIGPAHPKYA     106

Qy   181 TEAARLATFKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKDWESDDVPWEQHA 240
         ||:|||  |:||||:|:|||||:|:|||||||:|||||||||||||:||||||||||||
Db   107 HEAARVKSFHNWPRCMKQRPEQMADAGFFYTGYGDNTKCFYCDGGLKDWEPEDVPWEQHV 166

Qy   241 RWFDRCAYYQLVKGRDYIQKVKSEATAI---SASEEEQAATNDSTKNVAQEGEKHLDDSK 297
         |||||||||||||||:|::|:|            :|||||:|:||||||:||||:||||||
Db   167 RWFDRCAYYQLVKGRDYVQKVITEACVLPGENTVSTAAPVSEPIPETKIEKEPQVEDSK  226

Qy   298 ICKICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFNAVRLYFS 346
         |||||||  || ||||||||||||||||  ||  ||||||||||||||
Db   227 LCKICVEECIVCFVPCGHVVACAKCALSVDKCPMCRKIVTSVLKYFS  275
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```
Db   227 LCKICVEECIVCFVPCGHVVACAKCALSVDKCPMCRKIVTSVLKYFS 275
```

RESULT 3
US-08-836-134-21
; Sequence 21, Application US/08361344A
; Patent No. 6020127
; GENERAL INFORMATION:
; APPLICANT: Mackenzie, Alex E.
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mahadevan, Mani S.
; APPLICANT: McLean, Michael
; APPLICANT: Roy, Natalie
; APPLICANT: Ikeda, Joh-e
; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
; Patent No. 6020127
; TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
; FILE REFERENCE: 3477-112, 033477/139914
; CURRENT APPLICATION NUMBER: US/08/836,134A
; CURRENT FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Cydia pomonella
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-08-836-134-21

Query Match   51.2%; Score 966; DB 3; Length 275;
Best Local Similarity   59.2%; Pred. No. 1e-92;
Matches   171; Conservative 39; Mismatches 55; Indels 24; Gaps 3;

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Qy    68 MPDMREEERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCCAFCKVEIMRWVEGDDPA 127
         |:|||||||||||||:||||:||:|||||||||||||||||||||||||:||||||||||
Db     1 MSDLRLEEVRLNTFEKWPVSFLSPETMAKNGFYYLGRSDEVRCAFCKVEIMRWKEGEDDA  60

Qy   128 ADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAATQ------PPRMPGVHARYS 180
         |||:||:|||||:|:                :|||||:||:|||||||:|:
Db    61 ADHKKWAPQCPFVK----------GIDVCGSIVTLNNIQNTTHDTIIGPAHPKYA     106

Qy   181 TEAARLATFKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKDWESDDVPWEQHA 240
         ||:|||  |:||||:|:|||||:|:|||||||:|||||||||||||:||||||||||||
Db   107 HEAARVKSFHNWPRCMKQRPEQMADAGFFYTGYGDNTKCFYCDGGLKDWEPEDVPWEQHV 166

Qy   241 RWFDRCAYYQLVKGRDYIQKVKSEATAI---SASEEEQAATNDSTKNVAQEGEKHLDDSK 297
         |||||||||||||||:|::|:|            :|||||:|:||||||:||||:||||||
Db   167 RWFDRCAYYQLVKGRDYVQKVITEACVLPGENTVSTAAPVSEPIPETKIEKEPQVEDSK  226

Qy   298 ICKICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFNAVRLYFS 346
         |||||||  || ||||||||||||||||  ||  ||||||||||||||
Db   227 LCKICVEECIVCFVPCGHVVACAKCALSVDKCPMCRKIVTSVLKYFS  275
```

RESULT 4
US-09-493-784-21
; Sequence 21, Application US/09493784
; Patent No. 6429011
; GENERAL INFORMATION:
; APPLICANT: Mackenzie, Alex E.
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mahadevan, Mani S.
; APPLICANT: McLean, Michael
; APPLICANT: Roy, Natalie
; APPLICANT: Ikeda, Joh-e
; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
; Patent No. 6429011
; TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
; FILE REFERENCE: 3477-112, 033477/139914
; CURRENT APPLICATION NUMBER: US/09/493,784
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 08/836,134

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: January 6, 2005, 19:39:50 ; Search time 154 seconds
                                           (without alignments)
                                           805.976 Million cell updates/sec

Title: US-10-041-859-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAAATLVWLKN.........TDKCPMCRRFTNAVRLYFS 346
Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_23Sep04:*
                1: geneseqp1980s:*
                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match length	DB	ID	Description
1	1887	100.0	346	5	ABB78046	Abb78046 Amino aci
2	1311	69.5	377	4	AAE07881	Aae07881 Fall army
3	767.5	40.7	263	5	ABB09488	Abb09488 AmEPV bac
4	721.5	38.2	438	4	AAB48189	Aab48189 Drosophil
5	719.5	38.1	438	4	ABB61858	Abb61858 Drosophil
6	719.5	38.1	438	4	ABB67347	Abb67347 Drosophil
7	719.5	38.1	438	4	AAB48188	Aab48188 Drosophil
8	719.5	38.1	438	8	AAB48190	Aab48190 Drosophil
9	719.5	38.1	438	4	ADO08093	Ado08093 Fly polyp
10	713.5	37.8	438	4	AAB48192	Aab48192 Drosophil
11	713.5	37.8	438	4	AAB48191	Aab48191 Drosophil
12	711.5	37.7	438	4	AAB48196	Aab48196 Drosophil
13	709.5	37.6	438	4	AAB48197	Aab48197 Drosophil
14	708.5	37.5	438	4	AAB48193	Aab48193 Drosophil
15	708.5	37.5	438	4	AAB48194	Aab48194 Drosophil
16	532.5	28.2	434	4	AAB48195	Aab48195 Drosophil
17	526.5	27.9	604	2	AAW19747	Aaw19747 Human inh
18	526.5	27.9	604	2	AAW13546	Aaw13546 Human c-I
19	526.5	27.9	604	2	AAY52703	Aay52703 Human cel
20	526.5	27.9	604	2	AAY33997	Aay33997 Human cel
21	526.5	27.9	604	6	ABU07431	Abu07431 Protein d
22	526.5	27.9	604	7	ABB82739	Abb82739 Human CIA
23	526.5	27.9	604	6	ADB80948	Adb80948 RING-SH c
24	526.5	27.9	604	7	AAE39811	Aae39811 Human cel
25	526.5	27.9	604	8	ADG87135	Adg87135 Human CIA
26	526.5	27.9	604	8	ADH74643	Adh74643 Human cIA
27	525.5	27.8	600	2	AAW69298	Aaw69298 Murine HI
28	525.5	27.8	600	2	ABP72155	Abp72155 Mouse inh
29	524.5	27.8	604	2	AAW19582	Aaw19582 Human apo
30	524.5	27.8	604	2	AAW69295	Aaw69295 Human HIA
31	524.5	27.8	604	2	ABG65664	Abg65664 Human inh
32	517.5	27.4	602	2	ABG65667	Abg65667 Mouse inh
33	516.5	27.4	602	2	AAW19585	Aaw19585 Human apo
34	507.5	26.9	618	2	AAW19583	Aaw19583 Human apo
35	507.5	26.9	618	2	AAW69296	Aaw69296 Human HIA
36	507.5	26.9	618	7	ABG65665	Abg65665 Human inh
37	501	26.6	497	7	ADI39803	Adi39803 Drosophil
38	500.5	26.6	496	2	ADI39803	Adi39803 Mouse inh
39	500.5	26.5	618	2	AAW19745	Aaw19745 Human inh
40	500.5	26.5	618	2	AAW19746	Aaw19746 Human inh
41	500.5	26.5	618	2	AAW13545	Aaw13545 Human c-I
42	500.5	26.5	618	6	AAY33998	Aay33998 Human cel
43	500.5	26.5	618	7	ABP72160	Abp72160 Human inh
44	500.5	26.5	618	7	ADB80949	Adb80949 RING-SH c
45	500.5	26.5	618	7	ABR84600	Abr84600 IAP1 prot
	500.5	26.5	618	7	ADD25639	Add25639 Binding d

ALIGNMENTS

RESULT 1
ABB78046
ID   ABB78046 standard; protein; 346 AA.
XX
AC   ABB78046;
XX
DT   22-OCT-2002 (first entry)
XX
DE   Amino acid sequence of inhibitor of apoptosis protein BmIAP.
XX
KW   Inhibitor of apoptosis protein; IAP; BmIAP; silkworm; apoptosis; insect;
KW   Spodoptera frugiperda; insult-resistant plant; caspase.
XX
OS   Bombyx mori.
XX
FH
FT   Key   Location/Qualifiers
FT   Domain   74. .140
FT   /note= "BIR domain 1"
FT   Domain   182. .249
FT   /note= "BIR domain 2"
FT   Domain   298. .314
FT   /note= "RING domain"
XX
PN   WO200253586-A2.
XX
PD   11-JUL-2002.
XX
PF   07-JAN-2002; 2002WO-US000314.
XX
PR   08-JAN-2001; 2001US-0260478P.
XX
PA   (BURN-) BURNHAM INST.
XX
PI   Maeda S, Huang Q, Reed JC, Deveraux QL;
XX
DR   WPI; 2002-590628/63.
DR   N-PSDB; ABQ78228.
XX
PT   Novel recombinant polypeptide, inhibitor of apoptosis protein family
PT   member BmIAP from silkworm Bombyx mori BmN cells, useful for inhibiting
PT   apoptosis and identifying an agent that modulates activity of
PT   polypeptide.
XX
PS   Claim 39; Page 31; 62pp; English.
XX
CC   The present score represents a polypeptide which is an inhibitor of
CC   apoptosis protein (IAP) family member, and designated BmIAP. BmIAP is
CC   derived from silkworm Bombyx mori BmN cells. The BmIAP polypeptide

CC   contains two baculoviral IAP repeat (BIR) domains, followed by a RING
CC   domain. BmIAP polypeptides and polynucleotides are useful for inhibiting
CC   apoptosis in insect cells, especially Spodoptera frugiperda or Bombyx
CC   mori cells, and mammalian cells, and plant cells. They are also useful
CC   for generating a biotic or abiotic insult-resistant plant. BmIAP is also
CC   useful for inhibiting caspases
XX
SQ   Sequence 346 AA;

Query Match   100.0%; Score 1887; DB 5; Length 346;
Best Local Similarity   100.0%; Pred. No. 5.7e-174;
Matches 346; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MELTKVAKNGAAATLVMLKNARDAKMRPFIGPLMLSSCESSTTSTLPSPSSSADKTDNHD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MELTKVAKNGAAATLVMLKNARDAKMRPFIGPLMLSSCESSTTSTLPSPSSSADKTDNHD 60

Qy   61 TFNFLPDMPDMRREERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCCAFCKVEIMRW 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TFNFLPDMPDMRREERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCCAFCKVEIMRW 120

Qy   121 VEGDDPAADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAATQPPRMPGPVHARYS 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 VEGDDPAADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAATQPPRMPGPVHARYS 180

Qy   181 TEAARLATFKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKDWESDDVPWEQHA 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TEAARLATFKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKDWESDDVPWEQHA 240

Qy   241 RWFDRCAYYQLVKGRDYIQKVKSEATAISASEEEQAATNDSTKNVAQEGEKHLLDDSKICK 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 RWFDRCAYYQLVKGRDYIQKVKSEATAISASEEEQAATNDSTKNVAQEGEKHLLDDSKICK 300

Qy   301 ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS 346

RESULT 2
AAE07881
ID   AAE07881 standard; protein; 377 AA.
XX
AC   AAE07881;
XX
DT   01-NOV-2001 (first entry)
XX
DE   Fall armyworm inhibitor of apoptosis (IAP) protein.
XX
KW   Fall armyworm; inhibitor of apoptosis; IAP; transgenic plant;
KW   apoptosis inhibitor; therapy; acquired immune deficiency syndrome; AIDS;
KW   neurodegenerative disease; Alzheimer's disease; aplastic anaemia;
KW   Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;
KW   myelodysplastic syndrome; toxin-induced liver disease; ischaemic injury;
KW   myocardial infarction; stroke; reperfusion injury; cancer; nootropic;
KW   autoimmune disorder; lupus erythematosus; multiple sclerosis; vasotropic;
KW   insecticide; viral infection; anti-HIV; human immunodeficiency virus;
KW   neuroprotective; antianaemic; cardiant; cerebroprotective; vulnerary;
KW   cytostatic; immunosuppressive; virucide; antialcoholic.
OS   Spodoptera frugiperda.
XX
CC   W020015910B-A2.

Query Match   100.0%; Score 1887; DB 5; Length 346;
Best Local Similarity   100.0%; Pred. No. 5.7e-174;
Matches 346; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MELTKVAKNGAAATLVMLKNARDAKMRPFIGPLMLSSCESSTTSTLPSPSSSADKTDNHD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MELTKVAKNGAAATLVMLKNARDAKMRPFIGPLMLSSCESSTTSTLPSPSSSADKTDNHD 60

Qy   61 TFNFLPDMPDMRREERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCCAFCKVEIMRW 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TFNFLPDMPDMRREERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCCAFCKVEIMRW 120

Qy   121 VEGDDPAADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAATQPPRMPGPVHARYS 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 VEGDDPAADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAATQPPRMPGPVHARYS 180

Qy   181 TEAARLATFKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKDWESDDVPWEQHA 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TEAARLATFKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLKDWESDDVPWEQHA 240

Qy   241 RWFDRCAYYQLVKGRDYIQKVKSEATAISASEEEQAATNDSTKNVAQEGEKHLLDDSKICK 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 RWFDRCAYYQLVKGRDYIQKVKSEATAISASEEEQAATNDSTKNVAQEGEKHLLDDSKICK 300

Qy   301 ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS 346
              ||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS 346

XX
DR   WPI; 2001-516667/56.
DR   N-PSDB; AAD14419.
XX
PT   Novel nucleic acid construct comprising cDNA encoding inhibitor of
PT   apoptosis proteins, useful for controlling apoptosis in target cells and
PT   for combating various disorders associated with apoptosis.
XX
CC   Claim 6; Page 39; 43pp; English.

The present sequence is fall armyworm inhibitor of apoptosis (IAP). The
IAP is useful for controlling apoptosis in target cells. It is also
useful for screening compounds that modulate apoptosis and for the
production of transgenic plants. The IAP can be used to delay, suppress
or inhibit an apoptosis response in plants. In animals, IAPs are used to
combat various disorders related to apoptosis, e.g., acquired
immunodeficiency syndrome (AIDS), neurodegenerative diseases (e.g.
Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis),
retinitis pigmentosa and other diseases of retina, myelodysplastic
syndrome (e.g. aplastic anaemia), toxin-induced liver diseases (e.g.
alcoholism), ischaemic injury (e.g. myocardial infarction, stroke and
reperfusion injury), cancers, autoimmune disorders (e.g. lupus
erythematosis and multiple sclerosis) and viral infections. The IAP is
also useful in vitro to monitor the expression of IAP cDNA, and to detect
and monitor the presence of IAPs in a sample. The IAP DNAs are used in
the construction of recombinant baculoviruses that are useful as
insecticides

SQ   Sequence 377 AA;

Query Match   69.5%; Score 1311; DB 4; Length 377;
Best Local Similarity   68.5%; Pred. No. 4.5e-118;
Matches 248; Conservative   39; Mismatches   57; Indels   18; Gaps   7;

Qy   1 MELTKVAKNGAAATLVMLKN-ARDAKMRPFIGPLML--SSCESSTTSTLPSPSS------ 51
              |:|||||:|||:|||| ||| :|||||||||||||| :|||||||||:|||||||
Db   18 MDITKVASNGSSSTLTLFKSGSLEAKIRP-LAPIMLPTPSYDSNAGSPSLSPSTPCSSSS 76

Qy   52 -SADKTDNHDTFNFLPDMPDMRREERLKTFDQWPVTFLTPEQLARNGFYYLGRGDEVCC 110
               ||||||||||||||||:||||||||||| |||:|:|||||||||||||||||||||| |
Db   77 FSIDKTDNHDTFGFSADTVDMRKEDERWKTFEKWPVSFLSGEQLARNGFYYLGRRDEARC 136

Qy   111 AFCKVEIMRWVEGDDPAADHRRWAPQCPFVRK-LNGTAAADTGSSGQDECGARAAPSGTS 167
              |||||||||||| ||||||||||||||||||| ||||||| ::||| ::||| ::
Db   137 AFCKVEIMRWVEGDDPAKDHQRWAPQCPFVRK-LNGTAAADTGSSGQDECGARAAPSGTS 195

Qy   168 PPRMPGPVHARYSTEAARLATFKDWPRRMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLK 227
              |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db   196 PPRMAGPVHPRYASEAARLRSFRDWPRCMRQKPEELAEAGFFYTGQGDKTKCFYCDGGLK 255

Qy   228 DWESDDVPWEQHARWFDRCAYYQLVKGRDYIQKVKSEATAISASEEEQ---AATNDSTKN 284
              ||:|:||||||| ||:|::|||||||||||:||||:|:::||:|::|| :|||||||
Db   256 DWENHDVPWEQHARWFDRCAYYQLVKGREYVQKVISEACEVSASEAERVAPARTAEPSP 315

Qy   285 VAQEGEKHLLDDSKICK-ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLY 344
              |||:||||||||||||| :|||||||||||||||||| :|||||||||||||||||||||||
Db   316 PAEAPENSVDDSKLCKICYAEERNVCFVPCGHVVACARCACPMCRRTFQNAVRLY 375

Qy   345 FS 346
              ||
Db   376 FS 377

RESULT 3
ABB09488
ID   ABB09488 standard; protein; 263 AA.
XX
AC   ABB09488;
XX
DT   01-JUL-2002 (first entry)
XX
DE   AmEPV baculovirus-like inhibitor of apoptosis (AMVI33).
XX

QM nucleic - protein search, using frame_plus_n2p model

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GenCore version 5.1.6

Run on: January 6, 2005, 20:01:33 ; Search time 674 Seconds
(without alignments)
6441.806 Million cell updates/sec

QM nucleic - protein search, using frame_plus_n2p model

Title: US-10-041-859-1
Perfect score: 6692
Sequence: 1 cattattaaactccacttcac.........tgcgggctctacttctcgtga 3773

Searched: 1825181 seqs, 575374646 residues

Scoring table: BLOSUM62
Xgapop 10.0 ; Xgapext 0.5
Ygapop 10.0 ; Ygapext 0.5
Fgapop   6.0 ; Fgapext 7.0
Delop   6.0 ; Delext   7.0

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum Match 100%

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10041859/runat_06012005_133739_3209/app_query.fasta_1.3911
-DB=UniProt_02 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US1041859_@CGN_1_718 @runat_06012005_133739_3209 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	1887	28.2	346	2	Q96T8	Q96T8 bombyx mori
2	1866	27.9	346	2	Q8IS31	Q8IS31 bombyx mori
3	1333.5	19.9	379	2	Q9U492	Q9U492 trichoplusi
4	1319	19.7	377	2	Q9NJ07	Q9NJ07 spodoptera
5	966	14.4	275	1	IAP_GVCP	P41436 cydia pomon
6	937	14.0	287	2	Q6E7G7	Q6E7G7 anticarsia
7	890.5	13.3	280	2	Q6VTV9	Q6VTV9 choristoneu
8	890.5	13.3	280	2	AAQ91688	AAQ91688 choriston
9	879	13.1	263	2	Q80SF4	Q80SF4 hyphantria
10	876	13.1	281	2	Q80SF4	Q80SF4 choristoneu
11	873	13.0	261	2	Q9YNL8	Q9YNL8 choristoneu
12	873	13.0	276	2	Q9QES9	Q9QES9 epiphyas po
13	862	12.9	268	2	O89744	O89744 buzura supp
14	782	11.7	268	1	IAP3_NPVOP	P41437 orgyia pseu
15	747.5	11.2	264	2	Q9EN27	Q9EN27 amsacta moo
16	728	10.9	289	2	Q7QJ55	Q7QJ55 anopheles g

RESULT 1
Q96T8

ID	Q96T8	PRELIMINARY;	PRT;	346 AA.
AC	Q96T8;			

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein.
GN Name=IAP;
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21240184; PubMed=11341966;
RA Huang Q., Deveraux Q.L., Maeda S., Stennicke H.R., Hammock B.D.,
RA Reed J.C.;
RT "Cloning and characterization of an inhibitor of apoptosis protein
RT (IAP) from Bombyx mori.";
RL Biochim. Biophys. Acta 1499:191-198(2001).
DR EMBL; AF281073; AAK57560.1; -.
DR HSSP; Q24306; 1JD4.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 346 AA; 38942 MW; 6CFC6CC646894C69 CRC64;

ALIGNMENTS

17	728	10.9	313	2	Q9J827	Q9J827 spodoptera
18	723.5	10.8	438	1	IAP1_DROME	Q24306 drosophila
19	719.5	10.8	438	2	Q9VUX5	Q9VUX5 drosophila
20	701	10.5	403	2	Q8WRD9	Q8WRD9 aedes trise
21	684	10.2	401	2	Q6Q507	Q6Q507 aedes aegyp
22	684	10.2	401	2	AAS66751	AAS66751 aedes aeg
23	676.5	10.1	402	2	Q8T621	Q8T621 aedes albop
24	662	9.9	285	2	Q8JM16	Q8JM16 mamestra co
25	653	9.8	276	2	Q71A73	Q71A73 mamestra co
26	653	9.8	276	2	Q80L95	Q80L95 mamestra co
27	653	9.8	276	2	AAQ11158	AAQ11158 mamestra
28	635	9.5	283	2	Q80LK8	Q80LK8 adoxophyes
29	573	8.6	254	2	Q7T9S6	Q7T9S6 adoxophyes
30	544.5	8.1	269	2	Q6XJ6	Q6QXJ6 agrotis seg
31	544.5	8.1	269	2	AAS82685	AAS82685 agrotis s
32	542	8.1	358	1	PIAP_PIG	062640 sus scrofa
33	532.5	8.0	268	2	Q9B232	Q9B232 helicoverpa
34	530.5	7.9	401	2	Q8JHV9	Q8JHV9 xenopus lae
35	529.5	7.9	268	2	Q77LW6	Q77LW6 helicoverpa
36	529.5	7.9	268	2	Q9IF18	Q9IF18 helicoverpa
37	528.5	7.9	602	2	Q9SSE9	Q9SSE9 rattus norv
38	526.5	7.9	604	1	BIR3_HUMAN	Q13489 homo sapien
39	526	7.9	604	2	Q6DDY3	Q6DDY3 xenopus lae
40	525.5	7.9	600	1	BIR3_MOUSE	O08863 mus musculu
41	522	7.8	604	2	Q6GLD7	Q6GLD7 xenopus tro
42	516.5	7.7	616	2	Q804E2	Q804E2 ictalurus p
43	514	7.7	628	2	Q8UWD2	Q8UWD2 brachydanio
44	514	7.7	647	2	Q7T0K2	Q7T0K2 brachydanio
45	514	7.7	654	2	O62M93	O62M93 brachydanio

Alignment Scores:

```
Pred. No.:                                          2.7e-155
Score:                                              1887.00          Length:              346
Percent Similarity:                                 100.00%          Matches:             346
Best Local Similarity:                              100.00%          Conservative:        0
Query Match:                                        28.20%           Mismatches:          0
DB:                                                                  Indels:              0
                                                                     Gaps:                0

US-10-041-859-1 (1-3773) x Q96BT8 (1-346)

Qy    206 ATGGAGTTGACGAAAGTTGCTAAAAATGGAGCTGCCGCGCCACGTTGGTGATGTTAAAAAT 265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGTTGACGAAAGTTGCTAAAAATGGAGCTGCCGCGCCACGTTGGTGATGTTAAAAAT 60
Qy      1 MetGluLeuThrLysValAlaLysAsnGlyAlaAlaAlaAlaThrLeuValMetLeuLysAsn 20

Qy    266 GCGCGGGATGCAAAAATGCGACCTTTCATTGGTCCGCTCATGTTATCCTCGTGTGAGTCT 325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40

Qy    326 TCAACGACATCCACACTCCCGTCACCTTCGTCGTCGATAAAACGGATAATCACGAC 385
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41 SerThrThrSerThrLeuProSerProSerSerAlaAspLysThrAspAsnHisAsp 60

Qy    386 ACATTCAACTTCCTTCCTGATATGCCCGACATGGGTCGTGGTGAAGAGGGAACGTCTGAAAACA 445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ThrPheAsnPheLeuProAspMetProAspMetArgArgGluGluGlyThrSerGluThr 80

Qy    446 TTTGATCAGTGGCCCGGTTACGTTTTTGACCGCGGAACAATTGCCCCGCCAACGGATTCTAC 505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 PheAspGlnTrpProValThrPheLeuThrProGluGlnLeuAlaArgAsnGlyPheTyr 100

Qy    506 TACCTCGGTGCTGCGGGACGAAGTGTGCTGCTTTCTGTAAGGTAGAAAATTATGAGGTGG 565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 TyrLeuGlyArgGlyArgSerValCysCysAlaPheCysLysValGluIleMetArgTrp 120

Qy    566 GTCGAAGGGACGACGAATCCTCCCGCCGATCATCGGAGATGGGCGCGCCCCACGTGTCCCTTTGTA 625
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ValGluGlyAspAspProAlaAlaAspHisArgArgTrpAlaProGlnCysProPheVal 140

Qy    626 CGAAAAACAAAATGTATGCCAACGCTGGGGGAGGAGGCGGACACCGTCGGTGTAGACGCAATGT 685
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 ArgLysGlnMetTyrAlaAsnAlaGlyGlyGlyAlaThrAlaValGlyArgAspGluCys 160

Qy    686 GGGGGCCAGTGCGGCCCACGCAGCCTCCCCGGCGATGCCCGGCGCCGGTACTCC 745
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 GlyAlaSerAlaAlaThrGlnProProAlaArgMetProGlyProValHisAlaArgTyrSer 180

Qy    746 ACCGAGGCCGCGGCGCTCCCCACCTTCAAGGACTGGGCCGGAGCGTATCCGCCAAAAACCC 805
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ThrGluAlaAlaArgLeuAlaThrPheLysAspTrpProArgArgMetArgGlnLysPro 200

Qy    806 GAGGAAACTGGCAGAGGGCCGGAATTCTTCTATACAGGCCAAGGTGACAAAACGAAATGCTTC 865
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 GluGluLeuAlaGluAlaGlyPhePheTyrThrGlyGlnGlyAspLysThrLysCysPhe 220

Qy    866 TATTGCGACGGGAGGGGCTAAAAAGATTGGGAGAAGCGGATGAGAGGTTCCGTGGGAACAGCACGCC 925
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 TyrCysAspGlyLeuLysLysAspTrpGluSerAspAspValProTrpGluGlnHisAla 240

Qy    926 AGATGGTTCGACCCGCTACGTGCAAATTGGTGAAAGGAGACGTGACTACATTCAGAAG 985
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ArgTrpPheAspArgCysAlaTyrValGlnLeuValLysGlyArgArgAspTyrIleGlnLys 260

Qy    986 GTGAAGTCGGAGGCCACTGCGATATCTCGTAGGGAAGAAGACAGGCGCGCCACCAATGAT 1045
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 ValLysSerGluAlaThrAlaIleSerAlaSerGluGluGlnArgGlyAlaThrAsnAsp 280

Qy   1046 TCGACTAAGAACGTCGCCCAAGAGGGCGAGAAACATTGGATGACTCTAAAATATGTAAA 1105
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    281 SerThrLysAsnValAlaGlnGluGlyGluLysHisLeuAspAspSerLysLysCysLys 300

Qy   1106 ATATGTTATTCCCAGGAACGTAACGTTGTGTCTTCGTGCGCCGCCCACGTGTGGGCCTGC 1165
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 IleCysTyrSerGluArgAsnValCysPheValProCysGlyAlaHisValValAlaCys 320
```

```
Qy   1166 GCCAAGTGCGCCGCTCGTACGGACGAAGAAGTGCCCGATGTGTCGCAGAGACGTTCACGAATGCG 1225
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 AlaLysCysAlaAlaLeuSerThrAspGluGluValProAspValSerArgArgPheThrAsnAla 340

Qy   1226 GTGCGGCGCTCTTACTTCTCG 1243
          |||||||||||||||||||||
Db    341 ValArgLeuTyrPheSer 346
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```
RESULT 2
Q8IS31
Q8IS31
ID   Q8IS31;                        PRELIMINARY;      PRT;    346 AA.
AC   Q8IS31;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Inhibitor of apoptosis protein.
OS   Bombyx mori (Silk moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC   Bombycidae; Bombyx.
OX   NCBI_TaxID=7091;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yang G., Wang L., Wu X.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY155274; AAN46650.1; -.
DR   HSSP; Q24306; 1JD4.
DR   GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006916; P:anti-apoptosis; IEA.
DR   GO; GO:0016567; P:protein ubiquitination; IEA.
DR   InterPro; IPR001370; BIR.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00653; BIR; 2.
DR   SMART; SM00238; RING; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS01282; BIR_REPEAT_1; 2.
DR   PROSITE; PS50143; BIR_REPEAT_2; 2.
DR   PROSITE; PS00089; ZF_RING_2; 1.
SQ   SEQUENCE   346 AA;  38849 MW;  5450EB75F56A8486 CRC64;
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Alignment Scores:
Pred. No.:                                          1.83e-153
Score:                                              1866.00          Length:              346
Percent Similarity:                                 99.13%           Matches:             343
Best Local Similarity:                              99.13%           Conservative:        0
Query Match:                                        27.88%           Mismatches:          3
DB:                                                                  Indels:              0
                                                                     Gaps:                0

US-10-041-859-1 (1-3773) x Q8IS31 (1-346)

Qy    206 ATGGAGTTGACGAAAGTTGCTAAAAATGGAGCTGCCGCGCCACGTTGGTGATGTTAAAAAT 265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MetGluLeuThrLysValAlaLysAsnGlyAlaAlaAlaAlaThrLeuValMetLeuLysAsn 20

Qy    266 GCGCGGGATGCAAAAATGCGACCTTTCATTGGTCCGCTCATGTTATCCTCGTGTGAGTCT 325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40

Qy    326 TCAACGACATCCACACTCCCGTCACCTTCGTCGTCGATAAAACGGATAATCACGAC 385
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41 SerThrThrSerThrLeuProSerProSerSerAlaAspLysThrAspAsnHisAsp 60

Qy    386 ACATTCAACTTCCTTCCTGATATGCCCGACATGGGTCGTGGTGAAGAGGGAACGTCTGAAAACA 445
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ThrPheAsnPheLeuProAspMetProAspMetArgArgGluGluGlyThrSerGluThr 80

Qy    446 TTTGATCAGTGGCCCGGTTACGTTTTTGACCGCGGAACAATTGCCCCGCCAACGGATTCTAC 505
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 PheAspGlnTrpProValThrPheLeuThrProGluGlnLeuAlaArgAsnGlyPheTyr 100

Qy    506 TACCTCGGTGCTGCGGGACGAAGTGTGCTGCTTTCTGTAAGGTAGAAAATTATGAGGTGG 565
```

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: January 12, 2005, 18:42:28 ; Search time 10879 Seconds
                  (without alignments)
                  12637.844 Million cell updates/sec

Title: US-10-041-859-1
Perfect score: 3773
Sequence: 1 cattattaaactccacttcac........tgcggctcactcctcgtga 3773

Scoring table: IDENTITY_NUC
                  Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 1821986590B residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   EST:*
          1: gb_est1:*
          2: gb_est2:*
          3: gb_htc:*
          4: gb_est3:*
          5: gb_est4:*
          6: gb_est5:*
          7: gb_est6:*
          8: gb_gss1:*
          9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

```
Result                Query
No.    Score    Match Length   DB   ID          Description
-----  -------  ------------   --   --------    -----------
  1    705.6    712            5    BP121000    BP121000
  2    685.0    727            5    BP120885    BP120885
  3    683      723            1    AV401669    AV401669
  4    649.4    676            7    CK485834    rswab0_00
  5    639.8    658            7    CK505037    rswcc0_00
  6    588.4    612            7    CK518109    rswjb0_00
  7    577      624            7    CK564268    rswpb0_00
  8    549.4    575            7    CK514550    rswjb0_00
  9    546.6    633            7    CK495885    rswbb0_00
 10    521.4    622            7    CK497882    rswbb0_00
 11    502.8    549            7    CK544469    rswbb0_00
 12    502.4    512            5    AV398511    AV398511
 13    455.8    555            5    BP121882    BP121882
 14    453.0    489            7    CK494236    rswbb0_00
 15    449.6    459            7    CK500174    rswbb0_01
 16    438.6    500            5    BP115618    BP115618
 17    428.0    470            1    AV400060    AV400060
 18    293.6    522            9    CK516014    rswjb0_00
 19    179.6    804            7    CG786123    CM_MBa-76
 20    121.8    130            7    CK496041    rswbb0_00
 21    121      691            4    BM588815    17000687J
 22    114      712            9    BM601939    17000687O
 23    112.4    1896           9    CG753083    P048-1-C0
 24    108.8    727            7    CF525095    AGENCOURT
```

```
        Query
No.    Score   Match Length  DB  ID         Description
 c 25  105.6   592           2   BB978623   BB978623   b80h08.y
   26  105.2   937           6   CA981608   CA981608   AGENCOURT
   27  104.4   1489          9   AG350139   AG350139   Mus muscu
   28  104     678           6   CA805412   CA805412   ESG0118a.
 c 29  102.4   1101          9              CNS00EVL   Drosophil
 c 30  102.2   1539          9   AG340947   AG340947   Mus muscu
   31  102     633           1   AL854604   AL854604   Mus muscu
   32  102     636           1   AL872470   AL872470   Mus muscu
   33  101.8   644           1   AL854961   AL854961   Mus muscu
 c 34  101.8   2079          3   CB699915   CB699915   Mus muscu
   35  100.8   782           6   AG320553   AG320553   Mus muscu
   36  100.2   1780          9   CG753083   CG753083   P048-1-CO
 c 37  98.8    1896          9   CR729221   CR729221   Tetraodon
   38  98      1347          2   BM627420   BM627420   17000687A
   39  97.8    665           4   CK997149   CK997149   ip15c02.b
 c 40  96.8    1313          7   AG340947   AG340947   Mus muscu
 c 41  96.2    1539          1   AL855943   AL855943   Mus muscu
 c 42  95.6    626           1   AL855943   AL855943   Mus muscu
   43  95.6    1592          6   CG750135   CG750135   P044-3-DO
   44  95.4    910           6   CA981958   CA981958   AGENCOURT
 c 45  95.2    2087          9   AG333887   AG333887   Mus muscu
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ALIGNMENTS

RESULT 1
BP121000
LOCUS   BP121000   712 bp   mRNA   linear   EST 16-MAY-2003
DEFINITION BP121000 ceN- Bombyx mori cDNA clone ceN-4016, mRNA sequence.
ACCESSION   BP121000
VERSION   BP121000.1 GI:29554042
KEYWORDS   EST.
SOURCE   Bombyx mori (domestic silkworm)
ORGANISM   Bombyx mori
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
            Bombycoidea; Bombycidae; Bombyx.
REFERENCE   1 (bases 1 to 712)
AUTHORS   Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
TITLE   Bombyx mori cDNA (Mita,K. 2003)
JOURNAL   Unpublished (2003)
COMMENT   Contact: Mita K
            National Institute of Agrobiological Sciences
            Genome Research Group
            Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
            Email: kmita@nias.affrc.go.jp
            method:uni-directional; sequence direction:sequenced from T3 primer
            (5' -> 3').
FEATURES   Location/Qualifiers
     source   1..712
                     /organism="Bombyx mori"
                     /mol_type="mRNA"
                     /db_xref="taxon:7091"
                     /clone="ceN-4016"
                     /tissue_type="compound eye"
                     /clone_lib="ceN-"
                     /note="mixed stages from 5th instar larva to pupa"
ORIGIN

Query Match   18.7%; Score 705.6; DB 5; Length 712;
Best Local Similarity   99.4%;
Matches 708; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   665 GCTGTCGGTAGAGACGAAATGTGGGGCCAGTGGGGCCACGACCTCCCCGCATGCCCGCGC 724
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GCTGTCGGTAGAGACGAAATGTGGGGCCAGTGGGGCCACGACCTCCCCGCATGCCCGCGC 60

Qy   725 CCCGTGCACGCGCCGGGTACTCCACCGAGGCCGCGCGGGCGGCGGCGTTCGCCACCTTCAAGGACTGCCG 784
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCCGTGCACGCGCCGGGTACTCCACCGAGGCCGCGCGGGCGGCGGCGTTCGCCACCTTCAAGGACTGCCG 120

Qy   785 AGACGTATGCGCCCAAAAACCCGAGGAACTGGCAGAGAGGCCGGATTCTTCTATACAGGCCAA 844

ORIGIN

```
Db   121 AGATGTATGCCCCAAAAACCCGAGGAACTGGCGAGAGGCCGGATTCTTCTATACAGGCCAA 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   845 GGTGACAAAACGAAAATGCTTCTATTGTGCGACGGAGGGAGGCTAAAAGATTGGGAAAGGCCGGATGAC 904
```

```
Db   181 GGTGACAAAACGAAAATGCTTCTATTGTGCGACGGAGGGAGGCTAAAAGATTGGGAAAGGCCATGAC 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   905 GTTCCGTGGGAACAGCGACGCGCCAGATGGTTCGGACCCCTGGCGTTGCAATTGGTGAAA 964
```

```
Db   241 GTTCCGTGGGAACAGCGACGCGCCAGATGGTTCGGACCCCTGGCGTTGCAATTGGTGAAA 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   965 GGGACGTGACTTACATTCAGAAGGTGGAAGGTCGGAGGCCACTGGAGGCCGGATTCTTCT 1024
```

```
Db   301 GGGACGTGACTTACATTCAGAAGGTGGAAGGTCGGAGGCCACTGGAGGCCGGATTCTTCT 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1025 GAACAGGCCGCCCCACCCAAATGATTCGACTAAGAACGTCGCCCAAGAGGCCGAGAAACATTTG 1084
```

```
Db   361 GAACAGGCCGCCCCACCCAAATGATTCGACTAAGAACGTCGCCCAAGAGGCCGAGAAACATTTG 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1085 GATGACTCTAAAATATGTAAAATATGTTAATTCCGAGGAGGGGTAACCTCGAAATTGGTGAAA 1144
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Db   421 GATGACTCTAAAATATGTAAAATATGTTAATTCCGAGGAGGGGTAACGTCGTGTGCTTCGTGTGCCG 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1145 TGCGGGCCCACGTGGTGGGGTGCGCGTGCAAGTGGTCCGACGGACAAGTGCCCGATGTGT 1204
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```
Db   481 TGCGGGCCCACGTGGTGGGGTGCGCGTGCAAGTGGTCCGACGGACAAGTGCCCGATGTGT 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1205 CGCAGGACGTTCACGAAATGCGGGTGCGGGCGCTCTACTTCTCGTGAAAGGAGACCCTCCTCCGCGAG 1264
```

```
Db   541 CGCAGGACGTTCACGAAATGCGGGTGCGGGCGCTCTACTTCTCGTGAAAGGAGACCCTCCTCCGCGAG 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1265 CTGTATACTAATCACTTCACCGGGCGGCGCCCTGGAGCGTGCTCACAGAGGGGGAGAAACATTTG 1324
```

```
Db   601 CTGTATACTAATCACTTCACCGGGCGGCGCCCTGGAGCGTGCTCACAGAGGGGGAGAAACGA 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1325 AACCCGGTATCCTGTGATTTTTACATTAAATAAAATTACAAAATTGATAGCGG 1376
```

```
Db   661 AACCCGGTATCCTGTGATTTTTACATTAAATAAAATTACAAAATTGATAGCGG 712
```

RESULT 2

```
Query Match         18.2%;    Score 685.6;  DB 5;   Length 727;
Best Local Similarity  99.0%;    Pred. No. 1.1e-128;
Matches   721;   Conservative    0;  Mismatches   4;   Indels   3;   Gaps   3;
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```
Qy   665 GCTGTCGGTAGAGACGGAAGTGGGGGCCCAGTGCCGGCGGACCCTCCCCGGCGCCCGC 724
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GCTGTCGGTAGAGACGGAAGTGGGGGCCCAGTGCCGGCGGACCCTCCCCGGCATGCCCGGC 60
```

```
Qy   725 CCCGTGCACGCGCGCGGTACTCCACCGGGCGGCCTGCCCTCCCAAGGACTGGGCCG 784
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 CCCGTGCACGCGCGCGGTACTCCACCGGGCGGCCTGCCCTCCCAAGGACTGGGCCG 120
```

```
Qy   785 AGAGGTATGCGCCAAAAACCCGAGGAACTGGCGACGAGGCCGGATTCTTCTTATACAGGCCAA 844
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGATGTATGCGCCAAAAACCCGAGGAACTGGCGAGAGGCCGGATTCTTCTATACAGGCCAA 180
```

```
Qy   845 GGTGACAAAAACGAAAATGCTTCTATTGTGCGACGGAGGGAGGCTAAAAGATTGGGAAAGGCCGGATGAC 904
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGTGACAAAAACGAAAATGCTTCTATTGTGCGACGGAGGGAGGCTAAAAGATTGGGAAAGGCCATGAC 240
```

```
Qy   905 GTTCCGTGGGAACAGCGACGCGCCAGATGGTTCGGACCCCTGGCGTTGCAATTGGTGAAA 964
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GTTCCGTGGGAACAGCGACGCGCCAGATGGTTCGGACCCCTGGCGTTGCAATTGGTGAAA 300
```

```
Qy   965 GGGACGTGACTTACATTCAGAAGGTGGAAGGTCGGAGGCCACTGGAGGCCGGATTCTTCT 1024
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGGACGTGACTTACATTCAGAAGGTGGAAGGTCGGAGGCCACTGGAGGCCGGATTCTTCT 360
```

```
Qy  1025 GAACAGGCCGCCCACCCAAATGATTCGACTAAGAACGTCGCCCAAGAGGCCGAGAAACATTTG 1084
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAACAGGCCGCCCACCCAAATGATTCGACTAAGAACGTCGCCCAAGAGGCCGAGAAACATTTG 420
```

```
Qy  1085 GATGACTCTAAAATATGTAAAATATGTTAATTCCGAGGAGGGGTAACGTCGTGTGCTTCGTGTGCCG 1144
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GATGACTCTAAAATATGTAAAATATGTTAATTCCGAGGAGGGGTAACGTCGTGTGCTTCGTGTGCCG 480
```

```
Qy  1145 TGCGGGCCCACGTGGTGGGGTGCGCGTGCAAGTGGTCCGACGGACAAGTGCCCGATGTGT 1204
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGCGGGCCCACGTGGTGGGGTGCGCGTGCAAGTGGTCCGACGGACAAGTGCCCGATGTGT 540
```

```
Qy  1205 CGCAGGACGTTCACGAAATGCGGGTGCGGGCGCTCTACTTCTCGTGAAAGGAGACCCTCCTCCGCGAG 1264
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CGCAGGACGTTCACGAAATGCGGGTGCGGGCGCTCTACTTCTCGTGAAAGGAGACCCTCCTCCGCGAG 600
```

```
Qy  1265 CTGTATACTAATCACTTCACC-GGGCGCGGCGCCCTGGAGCGTGCTCACAGAGGGGGAAACACCC--TTCGAAC 1322
         ||||||||||||||||||||| ||||||||||||||||||||||||||||||| ||||||
Db   601 CTGTATACTAGTCACTTCACCGGGCGGCGCCCTGGAGCGTGCTCACAGAGGGGGAGAAACATTTG 660
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```
Qy  1323 GAAACCCGGTATCCTGTGATTTTTACATTAAATAAAATTACAAAATTGATAGCGGGTGGGGC 1382
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GAAACCCGGTATCCTGTGATTTTTACATTAAATAAAATTAC-AATTGATAGCGGGTGGGGC 719
```

```
Qy  1383 AATGTATA 1390
         ||||||||
Db   720 AATGTATA 727
```

RESULT 3

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: January 6, 2005, 20:44:23 ; Search time 121.5 Seconds
                 (without alignments)
                 5975.734 Million cell updates/sec

Title: US-10-041-859-1
Perfect score: 6692
Sequence: 1 cattattaaactccacttcac.........tgcggctacttctcgtga 3773

Scoring table: BLOSUM62
                 Xgapop   10.0 , Xgapext 0.5
                 Ygapop   10.0 , Ygapext 0.5
                 Fgapop   6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Qx/cgn2_1/USPTO_spool_p/US10041859//runat_06012005_133740_3222/app_query.fasta_1.3911
-DB=PIR_79 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -HEAPSIZE=500 -MINLEN=0 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -THR_MAX=100 -MAXLEN=200000000
-USER=US10041859 @CGN 1_1_188 @runat_06012005_133740_3222 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   PIR_79:*
        1:       pir1:*
        2:       pir2:*
        3:       pir3:*
        4:       pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	966	14.4	275	2	A45679	inhibitor-of-apott
2	862	12.9	268	2	T03183	inhibitor of apopt
3	862	12.9	268	2	T10304	apoptosis-inhibiti
4	542	8.1	358	2	A53989	apoptosis inhibito
5	524.5	7.8	604	2	JC5964	apoptosis inhibito
6	507.5	7.6	618	2	S68449	apoptosis inhibito
7	501	7.5	497	2	S68450	apoptosis inhibito
8	500.5	7.5	496	2	S69545	apoptosis inhibito
9	497.5	7.4	496	2	S69544	apoptosis inhibito
10	381.5	5.7	292	2	T41772	IAP1 orf27 - Bomby
11	378	5.6	286	2	D36828	orf13 protein - Au
12	369.5	5.5	275	2	T10310	apoptosis-inhibiti
13	367.5	5.5	298	2	JC7568	kidney inhibitor o
14	312	4.7	1447	2	T42628	neuronal apoptosis
15	302.5	4.5	1232	2	A55478	neuronal apoptosis
16	253	3.8	208	2	T03183	probable apoptosis
17	252.5	3.8	150	2	T28409	ORF MSV248 probabl
18	232	3.5	234	2	T30427	probable apoptosis
19	222.5	3.3	155	2	T30489	apoptosis inhibito
20	220.5	3.3	997	2	T43523	cut17 protein - fi
21	171.5	2.6	308	2	T37474	apoptosis inhibito
22	164.5	2.5	329	2	T28403	ORF MSV242 probabl
23	159.5	2.4	249	2	T41814	IAP2 orf71 - Bomby
24	159.5	2.4	249	2	H72858	apoptosis inhibito
25	159.5	2.3	4845	2	T31067	BIR repeat contain
26	156	2.3	236	2	T10343	inhibitor of apopt
27	155.5	2.3	383	2	F95582	hypothetical RING
28	149.5	2.2	115	2	B96664	probable RING zinc
29	139	2.1	124	2	T01251	hypothetical prote
30	139	2.1	489	2	S15349	mdm2 protein - mou
31	136.5	2.0	960	2	S72284	DNA-directed RNA p
32	132.5	2.0	864	2	T01393	apoptosis inhibito
33	130	1.9	428	2	T48167	hypothetical prote
34	124	1.9	960	2	S72284	DNA-directed RNA p
35	123.5	1.8	433	2	JC7678	RING finger protei
36	122.5	1.8	237	2	T52432	hypothetical prote
37	122.5	1.8	823	2	D86165	protein F15K9.3 [l
38	120	1.8	711	2	C84767	hypothetical prote
39	120	1.8	943	2	S68824	rngB protein, cyto
40	119	1.8	269	2	T40371	probable zinc fing
41	119	1.8	491	1	S24354	p53-binding protei
42	117	1.8	714	2	C90100	hypothetical prote
43	117	1.8	731	2	A99106	hypothetical prote
44	116.5	1.7	870	2	G86450	FSD14.31 protein -
45	116.5	1.7	1019	2	E90097	hypothetical prote

ALIGNMENTS

RESULT 1
A45679
inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV
C;Species: Cydia pomonella granulosis virus CpGV
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: A45679
R;Crook, N.E.; Clem, R.J.; Miller, L.K.
J. Virol. 67, 2168-2174, 1993
A;Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.
A;Reference number: A45679; MUID:93188168; PMID:8445726
A;Accession: A45679
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-275 <CRO>
A;Cross-references: UNIPROT:P41436; GB:L05494; NID:g2895583; PIDN:AAA43835.1; PID:g28958
A;Note: sequence extracted from NCBI backbone (NCBIN:127014, NCBIP:127015)
C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Alignment Scores:
Pred. No.:   1.03e-74   Length: 275
Score: 966.00   Matches: 171
Percent Similarity: 72.66%   Conservative: 39
Best Local Similarity: 59.17%   Mismatches: 55
Query Match: 14.44%   Indels: 24
DB: 2   Gaps: 3

US-10-041-859-1 (1-3773) x A45679 (1-275)

Qy   407 ATGCCCCGACACATGCGTCGGTGAAGGAGGAACGTCTGAAAACACATTTGATCAGTGGCCCGGTTACG 466
          |||||||:|||||||:||||| ::|||||||||||||||||||||||||||||||::
Db   1 MetSerAspLeuArgLeuGluGluValArgLeuAsnThrPheGluLysTrpProValSer 20

Qy   467 TTTTTGACGCGCGGAACAAATTGGCCCGCAACGGAGTTCTACTACCTCGGTCGCGAGGAA 526
          |||||||||:||||||||| :||||||||||||||||||||||||||||||||||
Db   21 PheLeuSerProGluThrMetAlaLysAsnGlyPheTyrTyrLeuGlyArgSerAspGlu 40

Qy   527 GTGTGCTGTGCTTTCTCTAAGGTAGAAAATTAYGAGGTGGGTGGCGAAGGCGACATCCTGCC 586
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||

Best Local Similarity: 54.55%
Percent Similarity: 65.82%
Score: 862.00
Pred. No.:
Score: 9.08e-66

Alignment Scores:

Mismatches: 72
Conservative: 31
Matches: 150
Length: 268

A;Status: preliminary; translated from GB/EMBL/DDBJ
F;217-261/Domain: RING finger homology <RRN>
A;Superfamily: viral apoptosis inhibitor IAP; RING finger homology
A;Cross-references: EMBL:U75930; NID:g2934903; PIDN:AAC59034.1; PID:g1911281
A;Residues: 1-268 <AHR>
A;Molecule type: DNA
A;Accession: T10304
A;Reference number: Z17011; MUID:97271300; PMID:9126251
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
Virology 229, 381-399, 1997
R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
C;Accession: T10304
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
inhibitor of apoptosis protein 3 - Orgyia pseudotsugata nuclear polyhedrosis virus
T10304
RESULT 2

Db 267 ThrSerValLeuLysValTyrPheSer 275

Db 247 ValAlaCysAlaLysCysSerAlaLeuSerValAspLysCysSerProMetCysArgGlyLysIleIleVal 266
Qy 1217 ACGAATGCGGTGCGGCGCTCTACTTCTCG 1243
Db 1217 ::|:::|||:::|||||||||||||||||

Qy 1157 GTGGCGTGGGCCAAGTGCGCCGCTGTCGACGGACAAAGTGCCCGAGATGTGTCGCGAGACGTTC 1216
Db 227 LeuCysLysLysIleCysTyrValGluGluCysArgIleValCysPheValProCysGlyHisVal 246
Qy 1097 ATATGTAAAATAGTTTATTATTCCGAGGAGGCGTAAGTGTGCTTGGTTCGTTGTGCCGTGCACGTG 1156

Db 207 ValSerGluProIleProGluThrLysIleGluGlyLysGlnValGluAspSerLys 226
Qy 1037 ACCAATGATTCGACTAAGAACGTCCCCCAAGAGGCGTAACGTGAACATTGGATGACTCTAAA 1096

Db 187 ValIleThrGluAlaCysValLeuProGlyValGlnAsnThrArgValSerThrArgAlaPro 206
Qy 986 GTGAAGTCGGAGGCCACTCGGATA 1036

Db 167 ArgTrpPheAspArgCysAlaLeuTyrValGlnLeuValLeuLysGlyLysArgAspTyrValGlnLys 186
Qy 926 AGATGGTTCGACCGCTGCGTACGTGCAATTGGTGAAGGACGTTGACTATTCAGAAG 985

Db 147 TyrCysAspGlyGlyLeuLysLysAspTrpGluProGlyValProTrpGluGlnHisVal 166
Qy 866 TATTGCGACGGAGGGCTAAAAGATTGGGAAGCCGGAGTTCCGTGGGAACAGCACGCC 925

Db 127 GluGlnMetAlaAspAlaGlyPhePheTyrThrGlyTyrGlyAspAsnThrArgCysPhe 146
Qy 806 GAGCAAATGCGACGAGAGCCGGATTCTTCTTACTACAGAGCCAAGGTGACAAAACGAAATGCTTC 865

Db 107 HisGluAlaAlaArgValLysSerPheHisAsnTrpProArgCysMetCysLysGlnArgPro 126
Qy 746 ACCGAGGCCGGCGGGCGCTTCGCCGACACTGGCCACCTTCAAGGACTGGCCCAAAACCC 805

Db   87 AsnIleGlnAsnThrThrThrHisAspThrIleLeuGluGlyProAlaHisProLysTyrAla 106
Qy 707 CCTCCCGGATGCCCCGTGCCCGGTCACGCGGGGTACTCC 745

Db   75 GlyIleLeuAspValCysGlySerIleValThrThrArgAsn 86
Qy 647 GCTGGGGGAGGAGGGCGACACCGCTGTCGTAGAGACGACGAATGTGGGGGCCCAGTGGGGCCCACGCAG 706

Db   61 AlaAspHisGlyLysTrpAlaProGlnCysProPheValLys 74

Db   41 ValArgCysAlaPheCysLysValGlnIleLeuMetArgTrpLysGluGlyGluAspProAla 60
Qy 587 GCCGATCATCCGAGAGTGGGGCGCCCCAGTGTCCCTTTGTAGAAAACAAAATGTATGCCAAC 646

DB:
Query Match: 12.88%   Indels: 22
2   Gaps: 2

US-10-041-859-1 (1-3773) x T10304 (1-268)

Db 252 CysProValCysArgGlyGlnLeuLeuAspLysCysAlaValAlaArgMetTyr 266
Qy 1193 TGCCCGAGTGTGTCGCGAGACGTTCACGGAAGTGCGGGTGCCGCTCTAC 1237

Db 232 CysPheValProCysGlyHisValValAlaAlaGlyLysValAlaGlyLysValThrThr 251
Qy 1133 TGCTTCGTTGTGCCGTGCCACGTGGTGGCCGCTGGGAAAGTGGCGGGTCTGACGGACAAG 1192

Db 212 GluValAlaGluValAlaAspAspArgLeuCysLysLeuCysSerLeuGlyAlaGlyThrVal 231
Qy 1073 GAGAAACATTGGAATGACTCTAAATATGTAAAAATATGTTATTCCGAGGAGGCGTAACGTG 1132

Db 199 AspIleAspAspAsnGluProHisIleGluArgProAlaVal 211
Qy 1013 GCTAGCGAAGAAGAAAACAGGCCGCCGCCACCAATGATTCGACTAAGAACGTCGCCCAAGAGGGC 1072

Db 179 LeuLeuValLysGlyArgAspPheValGlnArgValMetThrGluAlaCysValArg 198
Qy 953 CAATTGGTGAAAGGACGTTCACTACATTCAGAAGGTGAAGTCGGAGGCCACTGGGATATCT 1012

Db 159 GluProAspAspAlaProTrpGlnHisValAlaArgTrpTyrArgAspArgCysAspSerVal 178
Qy 893 GAAAGCGATGAGACGTTCCGTGGGAACAGCACGCCAGTGTGTTCGACGGTACGTG 952

Db 139 TyrThrGlyTyrGlnValGlyAspSerThrArgCysPheCysAspGlyLeuVal 158
Qy 833 TATACAGGCCCACAAGGTAGGACAAAACGAAATGCTTCTATTGCGACGGATTCTTC 892

Db 119 AlaGluTrpProArgGlyLeuCysLysGlnArgProGluGluLeuAlaGluAlaGlyPhePhe 138
Qy 773 AAGGACTGGCCGAGACGTATGCGCCCAAAAACCCGAGGAACACTGGCAGAGGCCGGATTCTTC 832

Db   99 AlaArgSerAlaAlaAlaLeuAlaHisProGlnIleTyrAlaThrGluAlaAlaArgThrPhe 118
Qy 713 CGCATGGCCCGCCCCGTCGCCCTGGCGCACTCCACCGAGCCGCGCCTTC 772

Db   94 AspArgAla 98

Db   74 HisLysArgTrpAlaProGlnCysProPheValArgAsnAsnAlaHisAspThrProHis 93
Qy 653 GGAGAGGCGACCCGCTGTCGGTAGGACGGAATGTGGGGGCCAGTGCGCCACGGAGCCTCCC 712

Db   54 CysAlaAlaPheCysLysValGluGlyIleLeuThrArgTrpLysAspAspAspProGluThrArgAsp 73
Qy 593 CATCGGAGATGGGGGGCGGCCCCAGTGTGTCCCTTTGTACGGAAACAAAATGTATGCCAAGGCTGGG 652

Db   34 GluProSerArgMetAlaAlaLeuSerGlyPheTyrTyrLeuGlyArgGlyAspGluValArg 53
Qy 533 TGTGCTTTTCTGTTAAGGGTAGAAAATTATGAGGTGGTTGCGAGAGGACGACGGATCTTGCCCCGAT 592

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RESULT 3
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apoptosis-inhibiting protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis vir
C;Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMNPV
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C;Accession: A53989
R;Birnbaum, M.J.; Clem, R.J.; Miller, L.K.
J. Virol. 68, 2521-2528, 1994
A;Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a polyp
A;Reference number: A53989; MUID:94187094; PMID:8139034
A;Accession: A53989
A;Status: preliminary

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: January 13, 2005, 08:49:51

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Perfect score: 3773
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Scoring table: IDENTITY_NUC
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Searched: 4300275 seqs, 2872944193 residues

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; Search time 1845 Seconds
(without alignments)

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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c 2	111.8	3.0	8056	18	US-10-473-126-386	Sequence 386, App
c 3	109.8	2.9	8056	18	US-10-473-126-386	Sequence 386, App
4	104	2.8	1317	16	US-10-267-502-202	Sequence 202, App
5	99.8	2.6	3673778	15	US-10-312-841-2	Sequence 2, Appli
6	95.5	2.5	8056	18	US-10-473-126-240	Sequence 240, Appli
c 7	94.6	2.5	5979	14	US-10-239-676-18	Sequence 18, Appl
c 8	94.6	2.5	5979	15	US-10-240-453-26	Sequence 26, Appl
c 9	94.2	2.5	8056	18	US-10-473-126-240	Sequence 240, App
10	93.2	2.5	74665	18	US-10-719-993-6854	Sequence 6854, Ap
11	91.8	2.4	843	14	US-10-244-586-2	Sequence 2, Appli
12	91.8	2.4	1068	15	US-10-203-708-21	Sequence 21, Appl
13	91.8	2.4	1168	16	US-10-188-646-12	Sequence 12, Appl
14	91.8	2.4	1260	15	US-10-188-646-4	Sequence 4, Appl
15	91.8	2.4	1268	18	US-10-807-897-28	Sequence 28, Appl
16	91.8	2.4	1322	18	US-10-807-897-26	Sequence 26, Appl
17	91.8	2.4	1337	14	US-10-235-026-1	Sequence 1, Appl
18	91.8	2.4	1363	18	US-10-839-882-37	Sequence 37, Appl
19	91.8	2.4	1376	14	US-10-239-676-18	Sequence 18, Appli
20	88.2	2.4	5979	15	US-10-244-586-1	Sequence 1, Appli
21	88.2	2.3	5979	15	US-10-240-453-26	Sequence 26, Appl
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ALIGNMENTS

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US-10-041-859-1
; Sequence 1, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2733)..(3770)
US-10-041-859-1

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GenCore version 5.1.6
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
US-09-502-528-1

; Sequence 1, Application US/09502528
; Patent No. 6570069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibitors of Apoptosis
; FILE REFERENCE: 023070-112000US
; CURRENT APPLICATION NUMBER: US/09/502,528
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1739
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; ORGANISM: Spodoptera frugiperda
; FEATURE:
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SfIAP) nucleotide sequence including 5' and 3'
; OTHER INFORMATION: untranslated regions, full length SfIAP cDNA
; NAME/KEY: CDS
; LOCATION: (229)..(1362)
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SfIAP)
US-09-502-528-1

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Matches 650; Conservative   0; Mismatches 262; Indels 21; Gaps 3;

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   504 GGACACAGTTGATATGAGAAAAGAGGATGAAACGTATGAAAACATTTGAAAAATGGCCCGT 563

Qy   463 TACGTTTTTGACGCCGCAGAACAATTGGCCCGCAACACGGATTCTACTACCTCGTCGCGGCGGA 522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   564 AAGTTTTCTTATCCGGAGAGCAACTGCTCGAAAAATGGATTTTACTACCTCGCCGGCCGTAGAGA 623

Qy   523 CGAAGTGTGCTGTGGTTGCTTTCTTGTAAGGTGAGAAATTATGAGGTGGGTCGAAGGGCACGATCC 582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   624 TGAAGCCCGTTGCGCTTTCTTGTAAAGTGCGAGATTATGAGGTGGGTGAGGGCCGATGACCC 683

Qy   583 TGCCGCCGATCATCGGAGGATGGGGCGCCCCAGTGTCCCTTTGTACGAAAAACAAATGTATGCC 642

```
Db   684  TGCGAAGGACCAATCAGGCGTTGGGCGCGCCACAGTGCCCATTGTTGTGCGCA---AATTGAACGG  740
          |||  || || | ||| || |||||  ||||  |  ||||  ||| ||||  |||     ||||||||
Qy   643  CAACGCTGGGGGAGGAGGCGACCACGCTGTCGTGAGAGACGGAATGTGGGCGCCAGTGCGGC---   699

Qy   741  TACTGCAGCAGCAGACACGGGTTCGGCGCCAGGACGAGGTGTGGTGCCCCGCGCCGCCTCC  800

Qy   700  ------CACGCAGCCTCCCGCCCATGCCGGGCGGGGGTACTCCACCGAGGC  753
          |||||||
Db   801  CTCCGGTACCTCTCCCGCCGGTATGCCGCGCCCCGGTCCCACGGGGCGGGGGTACTCCACCGAGGC  860

Qy   754  CGCGCGGCTCGGCCACCTTCAAGGACTGGCCAGACGTATGCCCAAAAACCCGAGGAACT  813
          |||||||||||||||||||||||||||||
Db   861  CGCACGACTACGCAGTTTTAAAGAGACTGGGCCACGACGATGCCACACAAAAAACCTGAAGAACT  920

Qy   814  GGCAGAGGCCCGGAATTCTTCTTCATATACAGGCCCGGACAAAACGAAATGCTTCTATTGTCGGA  873
          |||||||||||| ||  || |||| || |||
Qy   861  CCCCGGAGGCCTGGCCTTTTTTTTTACACTCGTCAGGGACAAAACCTTGTTTTTATTGCGA  920

Qy   874  CGGAGGGGCTAAAAAGAAATTGGGAAAGCGCAATGACGCCAAGACAGCACCAGCGATGGTT  933
          ||||||||||
Db   921  TGGTTGGATTAAAAGAATTGGGAGAACCATAGACGTACCCTGGGAACAACCACCCAAGTGGTT  980

Qy   934  CGGAGGGGCTAAAAAAGAATTGGGAAAGCGCAATGACGCCAAGACAGCACCAGCGATGGTT  933
Db   981  TGGTTGGATTAAAAGAATTGGGAGAACCATAGACGTACCCTGGGAACAACCACCCAAGTGGTT  1040

Qy   994  GGAGGGCCACTCGATATCTGCTTAGCGGAAGAAGAACAGG--------CGCCCACCAAATGA  1044
          |||||||
Db  1041  TGACCGTTGCGCCTACGTGCAATTGGTTGGACGTACCTTGAAGGGTCCGGAGAATACACCTGTTTTCC  1100

Qy  1045  TTCGGACTAAGAACGTCGCCCAAGAGGGGGCGAGAAAACATTTGGATGATGACTCTAAAAATATGTAA  1104
          |||||||||||||
Db  1101  TGAAGCTTGTGGAGGTTATCCGGGTTCAGAAGCGGCTCAGAGAAGCGGGCCGGAGCCACCGGACTGC  1160

Qy  1105  AAATATGTTATTCCGGAGGAGGCGGTAACGTGTGCTTCGTGTCCGTGGTGGGCGTG  1164
          |||||
Db  1161  CGAGCCAAGCCCGCGCCAGCAGCACGCGCCAGAAAACTCAGTGCTCGATGATGCGTGGTGGCTTG  1220

Qy  1165  CGCCAAGTGGCGCCGCTGTCGACGGACAAGTCCGGAGTTCTTCTATACAGGCCCAAGTGACAAAAACGAAATGCTTCTATTGCGA  1224
          |||||||
Db  1221  CGCCAAGTGGCGCCGCTGGGCGCCGACAAGTCGCCCATGTGCCGCGAGGACGTTTCAAAATGC  1280

Qy  1225  GGTGCGGCGCTCTACTTCTCGTGACGGACACCCTCC  1257
          |||||||
Db  1281  CGCCAAGTGGCGCCGCTGGGCGCCGACAAGTCGCCCATGTGCCGCGAGGACGTTTCAAAATGC  1340

Db  1341  AGTGCGGCGGTTATATTTTCCGTGACGGAGAGCCACC  1373
```

RESULT 2

```
Qy   343  CCCGTCACCTTCGTTGTCAGCTGATAAAAACGGATAATCAGACACACATTCAACTTCCTTCC  402
          |||||||||
Db   216  CTCTTCATCTTCTTTTCTCCCATTGATAAAACGACAACACACCTTCGGCTTCAGTGC  275

Qy   403  TGATAATGCCCGACATCGGTCGTCGTGAAGGAGGAACGTCTGAAGAACATTTGATCAGTGGGCCGT  462
          |||
Db   276  GGACAGAGTTGATATGAGAAAAAGAGGATGAACGTATGAAACATTTGAAAATGGCCCGT  335

Qy   463  TACGTTTTTGACGCCGGACAAATTGGCACCGAGTTCTACTACCTCGGTCGCGGCGGA  522
          |||||
Db   336  AAGTTTTCTTATCCGGAGGAGGAACGTGTCGGAGAGATTTTACTACCTCGGCCCGTAGAGA  395

Qy   523  CGAAGTGTGCTGCTGTGTTGCTTTCGTGTAACGGTAGAAAATTATGGAGGGGTCGGACGACGATCC  582
          ||||
Db   396  TGAAGCCCGTTGCGCGCTTTCTGTAAAGGTGGGGCCCCACAGTGGGGCCCGATCAGCCC  455

Qy   583  TGCCGCCGATCATCGGAGATGGGCCCCCCAGTGTTCCCTTTGTTACGAAAACAAATGTATGC  642
          |||||
Db   456  TGCGAAGGACCCATCAGCGTTGGGCGCGCCACAGTGCCCATTGTTGTGCGCA---AATTGAACGG  512

Qy   643  CAACGCTGGGGGAGGAGGCGACCGCTGTCGGTAGAGACGAAATGTGGGGGCGCCAGTGCGGC---  699
          |||||
Db   513  TACTGCAGCAGCAGACACGGGTTCCGGCCAGGACGAGGTGTGGTGCCCCGCGCCGCCTCC  572

Qy   700  ------CACGCAGCCTCCCGCCCATGCCGGGCGGGGGTACTCCACGGAGGC  753
          |||||||
Db   573  CTCCGGTACCTCTCCCGCCGGTATGCCGCGCCCCGGTCCCACGGGGCGGGGGTACTCCACGGAGGC  632

Qy   754  CGCGCGGCTCGGCCACCTTCAAGGACTGGCCAGACGTATGCGCCGGAAAAACCCCGGAGGAACT  813
          |||
Db   633  CGCACGACTACGCAGTTTAAAGAGACTGGGCCACGACGATGCCACAAAAAAACCTGAAGAACT  692

Qy   814  GGCAGAGGCCCGGAATTCTTCTATACAGGCCCAAGTGACAAAAACGAAATGCTTCTATTGCGA  873
          |||||
Db   693  CGCCCAGGCCTGGCCTTTTTTTTTACACTCGTCAGGGACAAAACCAAGTGTTTTTATTGCGA  752

Qy   874  CGGAGGGGCTAAAAGATTGGGAAAGCGCGATGACGTTCCGTGGGAACAGCAGCCAGATGGTT  933
          ||||
Db   753  TGGTTGGATTAAAAGAATTGGGAGAACCATAGACGTACCCTGGGAACAACCACCCAAGTGGTT  812

Qy   934  CGACCGCTGCGCCGGTACGTCCAATTGGTGAAAGGAGACGTGACTACATTCAGAAGGTGAAGTC  993
          |||
Db   813  TGACCGTTGCGCCCTACGTGCAATTGGTGAAAGGGTCGGAGAGATTTCTCAAAAGGTGATTTC  872

Qy   994  GGGAGGGCCACTCGATATCTGCTAGCGGAAGAAGAACAGG--------CGCCCACCAAATGA  1044
          |||||
Db   873  TGAAGCTTGTGGAGGTATCCGGGTTCAGAAGCGGAAGAACTGC  932

Qy  1045  TTCGGACTAAGAACGTCGCCCAAGAGGGGGCGAGAAAACATTTGGATGATGACTCTAAAAATATGTAA  1104
          ||||||||||||||
Db   933  CGAGCCAAGCCCGCGCCAGCAGCACGCGCCAGAAAACTCAGTCGATGAGACTCAAAAATGTAA  992

Qy  1105  AAATATGTTATTCCGGAGGAGGCGGTAACGTGTGCTTCGTGTCCGTGGGCCGCCACGTGGTGGGCGTG  1164
          |||||
Db   993  AATCTGTTATGCTGAAGAGCGTAACGTGTGCTTCGTGTCGGCGGCCACCTGGTGGGCCTTG  1052

Qy  1165  CGCCAAGTGGCGCCGCTGTCGACGGACAAGTGCCCGGAGTTCTTCTATACAGGCCCAAGTGACAAAAACGAAATGCTTCTATTGTGA  1224
          ||||||||||
Db  1053  CGCCAAGTGGCGCCGCTGGGCGCCGACAAGTGCCCCATGTGCCGCGAGGACGTTTCAAAATGC  1112

Qy  1225  GGTGCGGCGCTCTACTTCTCGTGA  1246
          ||||||||
Db  1113  AGTGCGGCGTTATATTTTCCGTGA  1134
```

RESULT 3

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: January 12, 2005, 16:43:28 ; Search time 1653 Seconds
(without alignments)
11981.891 Million cell updates/sec

Title: US-10-041-859-1
Perfect score: 3773
Sequence: 1 cattattaaactcacttcac..........tgcggctctacttccgtga 3773

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 262471052l residues
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn19808:*
2: geneseqn19908:*
3: geneseqn200s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3773	100.0	3773	6	ABQ78228	Abq78228 Nucleotid
2	441.8	11.7	1739	6	AAD14419	Aad14419 Fall army
c 3	142.4	3.8	50000	6	ABK28152	Abk28152 DNA trans
c 4	130.4	3.5	794	6	ABL55635	Abl55635 AmEPV gen
c 5	111.0	3.0	8056	8	ABZ10246	Abz10246 AmEPV bac
c 6	109.8	2.9	8056	8	ABZ10246	Abz10246 Haematopo
7	105.6	2.8	1304	5	AAC84527	Aac84527 Drosophil
8	105.6	2.8	1317	5	AAC84520	Aac84520 Drosophil
9	105.6	2.8	1317	5	AAC84529	Aac84529 Drosophil
10	105.6	2.8	1317	5	AAC84521	Aac84521 Drosophil
11	105.6	2.8	1317	5	AAC84525	Aac84525 Drosophil
12	105.6	2.8	1317	5	AAC84522	Aac84522 Drosophil
13	105.6	2.8	1317	5	AAC84526	Aac84526 Drosophil
14	105.6	2.8	1317	5	AAC84528	Aac84528 Drosophil
15	105.6	2.8	1317	5	AAC84524	Aac84524 Drosophil
16	104	2.8	1317	5	AAC84523	Aac84523 Drosophil
17	104	2.8	1317	12	ADO07876	Ado07876 Fly polyn
18	104	2.8	1858	4	ABL21061	Abl21061 Drosophil
19	104	2.8	2013	4	ABL21060	Abl21060 Drosophil
20	104	2.8	10432	4	ABL10083	Abl10083 Drosophil
21	104	2.8	14250	4	ABL21060	Abl21060 Drosophil
22	95.6	2.5	8056	8	ABZ10100	Abz10100 Haematopo
23	94.6	2.5	5979	4	AAS45313	Aas45313 Chemical1
24	94.6	2.5	5979	4	ABK28152	Abk28152 DNA trans
c 25	94.2	2.5	8056	8	ABZ10100	Abz10100 Haematopo
c 26	91.8	2.4	8056	8	ABZ10100	Abz10100 Haematopo
c 27	91.8	2.4	672	6	AAL42857	Aal42857 Survivin-
28	91.8	2.4	723	6	AAL42856	Aal42856 Survivin-
29	91.8	2.4	840	6	AAL42858	Aal42858 Survivin-
30	91.8	2.4	843	6	AAF24857	Aaf24857 Nucleotid
31	91.8	2.4	1068	4	AAD16364	Aad16364 Human SBh
32	91.8	2.4	1168	12	ADH89543	Adh89543 Human Liv
33	91.8	2.4	1260	12	ADH89535	Adh89535 Human Liv
34	91.8	2.4	1268	10	ACC72844	Acc72844 Human can
35	91.8	2.4	1322	10	ACC72843	Acc72843 Human can
36	91.8	2.4	1337	3	AAZ61210	Aaz61210 DNA encod
37	91.8	2.4	1363	3	AAA15007	Aaa15007 cDNA enco
c 38	90.4	2.4	1376	4	AAF24856	Aaf24856 Nucleotid
39	90.4	2.4	131680	10	ADF29092	Adf29092 Agrotis s
c 40	88.2	2.3	5979	6	AAS45313	Aas45313 Chemical1
41	88.2	2.3	5979	6	ABK28152	Abk28152 DNA trans
c 42	87.8	2.3	635	6	AAC95127	Aac95127 Cat flea
c 43	82	2.2	8310	2	AAZ29911	Aaz29911 cDNA enco
44	81	2.1	769	4	AAD16365	Aad16365 Human SBh
45	78.6	2.1	204	6	AAL42854	Aal42854 Survivin-
45	78	2.1	614	5	AAS91550	Aas91550 DNA encod

ALIGNMENTS

RESULT 1
ABQ78228

```
ID   ABQ78228 standard; cDNA; 3773 BP.
XX
AC   ABQ78228;
XX
DT   22-OCT-2002  (first entry)
XX
DE   Nucleotide sequence of inhibitor of apoptosis protein BmIAP.
XX
KW   Inhibitor of apoptosis protein; IAP; BmIAP; silkworm; apoptosis; insect;
KW   Spodoptera frugiperda; insult-resistant plant; caspase; gene; 88.
XX
OS   Bombyx mori.
XX
FH
FH   Key            Location/Qualifiers
FT
FT   CDS            2733..3773
FT                  /*tag= a
FT                  /product= "inhibitor of apoptosis protein BmIAP"
XX
PN   WO200253586-A2.
XX
PD   11-JUL-2002.
XX
PF   07-JAN-2002; 2002WO-US000314.
XX
PR   08-JAN-2001; 2001US-0260478P.
XX
PA   (BURN-) BURNHAM INST.
XX
PI   Maeda S,  Huang Q,  Reed JC,  Deveraux QL;
XX
DR   WPI; 2002-590628/63.
DR   P-PSDB; ABB78046.
XX
PT   Novel recombinant polypeptide, inhibitor of apoptosis protein family
PT   member BmIAP from silkworm Bombyx mori BmN cells, useful for inhibiting
PT   apoptosis and identifying an agent that modulates activity of
PT   polypeptide.
XX
PS   Claim 8; Page 29-30; 62pp; English.
XX
CC   The present score encodes a polypeptide which is an inhibitor of
CC   apoptosis protein (IAP) family member, and designated BmIAP. BmIAP is
```

```
CC   derived from silkworm Bombyx mori BmN cells. The BmIAP polypeptide
CC   contains two baculoviral IAP repeat (BIR) domains, followed by a RING
CC   domain. BmIAP polypeptides and polynucleotides are useful for inhibiting
CC   apoptosis in insect cells, especially Spodoptera frugiperda or Bombyx
CC   mori cells, and mammalian cells, and plant cells. They are also useful
CC   for generating a biotic or abiotic insult-resistant plant. BmIAP is also
CC   useful for inhibiting caspases
XX
SQ   Sequence 3773 BP; 1108 A; 785 C; 866 G; 1014 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 3773;  DB 6;  Length 3773;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3773;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATTATTAAACTCACTTCACTTCGGTAGTGTGAATGTTAACGTGAAACTCCGCGCTCTTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CATTATTAAACTCACTTCACTTCGGTAGTGTGAATGTTAACGTGAAACTCCGCGCTCTTC 60

Qy         61 TTTAGTTGCTACTCGGTTCTGTCTGGCTGCGTTGACGTTTTGGAACTTCATACTATTTTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTAGTTGCTACTCGGTTCTGTCTGGCTGCGTTGACGTTTTGGAACTTCATACTATTTTG 120

Qy        121 TTCTTGCAAGACGAGTGTCAGTGATTAAACAAAAACATAAGAATAGACGTTTTATGCGTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTCTTGCAAGACGAGTGTCAGTGATTAAACAAAAACATAAGAATAGACGTTTTATGCGTT 180

Qy        181 ACTAAAAAAAAGGAAAAATATACCAATGGAGTTGACGAAAGTTGCTAAAAATGGAGCTGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTAAAAAAAAGGAAAAATATACCAATGGAGTTGACGAAAGTTGCTAAAAATGGAGCTGC 240

Qy        241 CGCCACGTTGGTGATGTTAAAAAATGCGCGGGATGCAAAAATGCGACCTTTCATTGGTCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCCACGTTGGTGATGTTAAAAAATGCGCGGGATGCAAAAATGCGACCTTTCATTGGTCC 300

Qy        301 GCTCATGTTATCCTCGTGTGAGTCTTCAACGACATCCACACTCCCGTCACCTTCGTCGTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTCATGTTATCCTCGTGTGAGTCTTCAACGACATCCACACTCCCGTCACCTTCGTCGTC 360

Qy        361 AGCTGATAAAACGGATAATCACGACACATTCAACTTCCTTCCTGATATGCCCGACATGCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGCTGATAAAACGGATAATCACGACACATTCAACTTCCTTCCTGATATGCCCGACATGCG 420

Qy        421 TCGTGAAGAGGAACGTCTGAAAACATTTGATCAGTGGCCCGTTACGTTTTTGACGCCGGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCGTGAAGAGGAACGTCTGAAAACATTTGATCAGTGGCCCGTTACGTTTTTGACGCCGGA 480

Qy        481 ACAATTGGCCCGCAACGGATTCTACTACCTCGGTCGCGGCGACGAAGTGTGCTGTGCTTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACAATTGGCCCGCAACGGATTCTACTACCTCGGTCGCGGCGACGAAGTGTGCTGTGCTTT 540

Qy        541 CTGTAAGGTAGAAATTATGAGGTGGGTCGAAGGCGACGATCCTGCCGCCGATCATCGGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGTAAGGTAGAAATTATGAGGTGGGTCGAAGGCGACGATCCTGCCGCCGATCATCGGAG 600

Qy        601 ATGGGCGCCCCAGTGTCCCTTTGTACGAAAACAAATGTATGCCAACGCTGGGGGAGAGGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATGGGCGCCCCAGTGTCCCTTTGTACGAAAACAAATGTATGCCAACGCTGGGGGAGAGGC 660

Qy        661 GACCGCTGTCGGTAGAGACGAATGTGGGGCCAGTGCGGCCACGCAGCCTCCCCGCATGCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GACCGCTGTCGGTAGAGACGAATGTGGGGCCAGTGCGGCCACGCAGCCTCCCCGCATGCC 720

Qy        721 CGGCCCCGTGCACGCGCGGTACTCCACCGAGGCCGCGCGGCTCGCCACCTTCAAGGACTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGGCCCCGTGCACGCGCGGTACTCCACCGAGGCCGCGCGGCTCGCCACCTTCAAGGACTG 780

Qy        781 GCCGAGACGTATGCGCCAAAAACCCGAGGAACTGGCAGAGGCCGGATTCTTCTATACAGG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCGAGACGTATGCGCCAAAAACCCGAGGAACTGGCAGAGGCCGGATTCTTCTATACAGG 840

Qy        841 CCAAGGTGACAAAACGAAATGCTTCTATTGCGACGGAGGGCTAAAAGATTGGGAAAGCGA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCAAGGTGACAAAACGAAATGCTTCTATTGCGACGGAGGGCTAAAAGATTGGGAAAGCGA 900
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Qy        901 TGACGTTCCGTGGGAACAGCACGCCAGATGGTTCGACCGCTGCGCGTACGTGCAATTGGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGACGTTCCGTGGGAACAGCACGCCAGATGGTTCGACCGCTGCGCGTACGTGCAATTGGT 960

Qy        961 GAAAGGACGTGACTACATTCAGAAGGTGAAGTCGGAGGCCACTGCGATATCTGCTAGCGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAAAGGACGTGACTACATTCAGAAGGTGAAGTCGGAGGCCACTGCGATATCTGCTAGCGA 1020

Qy       1021 AGAAGAACAGGCCGCCACCAATGATTCGACTAAGAACGTCGCCCAAGAGGGCGAGAAACA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGAAGAACAGGCCGCCACCAATGATTCGACTAAGAACGTCGCCCAAGAGGGCGAGAAACA 1080

Qy       1081 TTTGGATGACTCTAAAATATGTAAAATATGTTATTCCGAGGAGCGTAACGTGTGCTTCGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTTGGATGACTCTAAAATATGTAAAATATGTTATTCCGAGGAGCGTAACGTGTGCTTCGT 1140

Qy       1141 GCCGTGCGGCCACGTGGTGGCGTGCGCCAAGTGCGCGCTGTCGACGGACAAGTGCCCGAT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GCCGTGCGGCCACGTGGTGGCGTGCGCCAAGTGCGCGCTGTCGACGGACAAGTGCCCGAT 1200

Qy       1201 GTGTCGCAGGACGTTCACGAATGCGGTGCGGCTCTACTTCTCGTGAAAGGACCCTCCTCG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GTGTCGCAGGACGTTCACGAATGCGGTGCGGCTCTACTTCTCGTGAAAGGACCCTCCTCG 1260

Qy       1261 CGAGCTGTATACTAATCACTTCACCGGGCGGCCCTGGAGCGTGCTGAAACCACCCTTCGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CGAGCTGTATACTAATCACTTCACCGGGCGGCCCTGGAGCGTGCTGAAACCACCCTTCGA 1320

Qy       1321 ACGAAACCGCGTATCCTGTGATTTTTACATTAAATAAATTTACAAATTGATAGCGGTGGG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACGAAACCGCGTATCCTGTGATTTTTACATTAAATAAATTTACAAATTGATAGCGGTGGG 1380

Qy       1381 GCAATGTATAGGAACTCGTCAGAACTCGCGAGTTGACGTGCAGGAAGGAGTTAGTGATTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCAATGTATAGGAACTCGTCAGAACTCGCGAGTTGACGTGCAGGAAGGAGTTAGTGATTT 1440

Qy       1441 GTAAACTTGTAAACTGATGTTGAAATGATTTTATTTATTATTTAAAATTCTAATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTAAACTTGTAAACTGATGTTGAAATGATTTTATTTATTATTTAAAATTCTAATGACAAA 1500

Qy       1501 GTGTAAGTAAATAAATGTACATATTATTTTAGATTATCAGTTTGTCCCACCGACAAAAGT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GTGTAAGTAAATAAATGTACATATTATTTTAGATTATCAGTTTGTCCCACCGACAAAAGT 1560

Qy       1561 GAAATGTACATAGGTGTTTTCATATCACTTCAACAGTCGAAGACCTTCTTTTTGAATTTA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GAAATGTACATAGGTGTTTTCATATCACTTCAACAGTCGAAGACCTTCTTTTTGAATTTA 1620

Qy       1621 AGGATATATATTTATACATATAAATTAAAATTTTAACGAGACATCAATATAAATGGTTTA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AGGATATATATTTATACATATAAATTAAAATTTTAACGAGACATCAATATAAATGGTTTA 1680

Qy       1681 ACAACTTATTTATACACTGAAATCAAGTGAAGTGTAACATGGTCTGAAGAATGTTTTACT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACAACTTATTTATACACTGAAATCAAGTGAAGTGTAACATGGTCTGAAGAATGTTTTACT 1740

Qy       1741 GATTTCACTTCCCCTGTTGAAGTGATAAAATTCTAATGTAAATCCAGAGTTTAAATGTCG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GATTTCACTTCCCCTGTTGAAGTGATAAAATTCTAATGTAAATCCAGAGTTTAAATGTCG 1800

Qy       1801 TCATAATTAATATAAGAAACAAGTTTTACGCTTCTTTTGCTTGAAAAATCTTATAATTGA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TCATAATTAATATAAGAAACAAGTTTTACGCTTCTTTTGCTTGAAAAATCTTATAATTGA 1860

Qy       1861 TTCAGGAATTATTTAATGTGACTATATTTTGTTCCTGTAAATAACATAATATATACTATT 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TTCAGGAATTATTTAATGTGACTATATTTTGTTCCTGTAAATAACATAATATATACTATT 1920

Qy       1921 TATTGATTAATTCTGACATAATTTATGGCAATTCCGTAAGATACAATCCAATACTTATTT 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TATTGATTAATTCTGACATAATTTATGGCAATTCCGTAAGATACAATCCAATACTTATTT 1980
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: January 6, 2005, 19:57:18 ; Search time 443 Seconds
                                            (without alignments)
                                            6141.921 Million cell updates/sec

Title: US-10-041-859-1
Perfect score: 6692
Sequence: 1 cattattaaactccacttcac..........tgcggctcacttctcgtga 3773

Scoring table: BLOSUM62
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               Ygapop   10.0 , Ygapext   0.5
               Fgapop   6.0 , Fgapext   7.0
               Delop   6.0 , Delext   7.0

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 3207808

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters: -DEV=xlp
-MODEL=frame+_n2p.model
-Q=/gn2_1/USPTO_spool_p/US10041859/runat_06012005_133738_3149/app_query.fasta_1.3911
-DB=Published_Applications_AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100
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-MAXLEN=200000000 -USER=US10041859 @CGN_1_1_545 @runat_06012005_133738_3149
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG - DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database :   Published_Applications_AA:*
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2:   /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3:   /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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6:   /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Result   #
                Query

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
1	1887	28.2	346	14	US-10-041-859-2	Sequence 2, Appli
2	966	14.4	275	9	US-09-201-936-12	Sequence 12, Appl
3	966	14.4	275	14	US-10-323-643-9	Sequence 9, Appl
4	966	14.4	275	16	US-10-600-272-12	Sequence 12, Appli
5	932.5	13.9	172	14	US-10-041-859-8	Sequence 8, Appl
6	862	12.9	268	14	US-10-323-643-10	Sequence 10, Appl
7	846.5	12.6	172	14	US-10-041-859-10	Sequence 10, Appl
8	831.5	12.4	172	14	US-10-041-859-9	Sequence 9, Appl
9	759.5	11.3	172	14	US-10-041-859-11	Sequence 11, App
10	719.5	10.8	438	15	US-09-974-592-6	Sequence 419, App
11	696.5	10.4	172	14	US-10-041-859-12	Sequence 12, Appl
12	554.5	8.3	172	14	US-10-041-859-13	Sequence 13, Appl
13	526.5	7.9	604	14	US-10-232-286-4	Sequence 4, Appli
14	526.5	7.9	604	14	US-10-141-618-6	Sequence 6, Appli
15	526.5	7.9	604	16	US-10-366-307-6	Sequence 6, Appli
16	526.5	7.9	604	16	US-10-730-476A-79	Sequence 79, Appl
17	526.5	7.9	604	17	US-10-825-282-40	Sequence 40, Appl
18	525.5	7.9	604	15	US-09-974-592-12	Sequence 12, Appl
19	525.5	7.9	600	17	US-10-482-952-1	Sequence 1, Appli
20	524.5	7.8	604	9	US-09-974-592-6	Sequence 6, Appli
21	524.5	7.8	604	16	US-09-201-936-6	Sequence 6, Appli
22	524.5	7.8	604	16	US-10-636-065-221	Sequence 221, App
23	524.5	7.8	602	16	US-10-600-272-6	Sequence 6, Appli
24	517.5	7.7	602	16	US-09-201-936-40	Sequence 40, App
25	517.5	7.7	602	16	US-10-636-065-227	Sequence 227, App
26	517.5	7.7	602	16	US-10-600-272-40	Sequence 40, Appl
27	507.5	7.6	618	9	US-09-974-592-8	Sequence 8, Appli
28	507.5	7.6	618	14	US-09-201-936-8	Sequence 8, Appli
29	507.5	7.6	618	16	US-10-636-065-223	Sequence 223, App
30	507.5	7.6	618	16	US-10-600-272-8	Sequence 8, Appli
31	500.5	7.5	498	16	US-09-201-936-13	Sequence 13, Appl
32	500.5	7.5	498	16	US-10-600-272-13	Sequence 13, Appl
33	500.5	7.5	618	14	US-10-153-668-338	Sequence 338, App
34	500.5	7.5	618	14	US-10-207-655-200	Sequence 200, App
35	500.5	7.5	618	14	US-10-232-286-2	Sequence 2, Appli
36	500.5	7.5	618	14	US-10-366-307-4	Sequence 4, Appli
37	500.5	7.5	618	15	US-10-361-270-3	Sequence 3, Appli
38	500.5	7.5	618	15	US-10-260-708-63	Sequence 63, Appl
39	500.5	7.5	618	15	US-10-730-476A-78	Sequence 78, Appl
40	499.5	7.5	618	17	US-10-482-952-11	Sequence 11, Appl
41	499.5	7.5	497	14	US-10-366-307-2	Sequence 2, Appli
42	497.5	7.4	497	9	US-09-974-592-4	Sequence 4, Appli
43	497.5	7.4	497	16	US-09-201-936-4	Sequence 4, Appli
44	497.5	7.4	497	16	US-10-636-065-219	Sequence 219, App
45	497.5	7.4	497	16	US-10-600-272-4	Sequence 4, Appli

ALIGNMENTS

US-10-041-859-2

Alignment Scores:
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Pred. No.:              4.1e-166      Length:        346
Score:                  1887.00       Matches:       346
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            28.20%        Indels:        0
DB:                     14            Gaps:          0
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US-10-041-859-1 (1-3773) x US-10-041-859-2 (1-346)

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Qy  206 ATGGAGTTGACGAAAGTTGCTAAAAATGGAGCTGCCGACGTTGGGTGAGTTAAAAAAT 265
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Db    1 MetGluLeuThrLysValAlaLysAsnGlyAlaAlaAlaThrLeuValMetLeuLysAsn 20

Qy  266 GCGCGGGATGCAAAAATGCAACCTTTCATTGGTCCGCTCATTGTTATCCTCGTGTGAGTCT 325
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40

Qy  326 TCAACGACATCCACACTCCCGTCACCTTCGTCGTCAGCTGATAAAACGGATAATCACGAC 385
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 SerThrThrSerThrLeuProSerProSerSerSerAlaAspLysThrAspAsnHisAsp 60

Qy  386 ACAATTCAACTTCCTTCCTGATATGCCCGACACATGGCTCTGTGAAGAGGAACGTCTCAAAACA 445
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ThrPheAsnPheLeuProAspMetProAspMetArgLeuCysGluGluGluArgLeuLysThr 80

Qy  446 TTTGATCCAGTGGCCCGTTACGTTTTTTGACCCGGAACAATTGGCCCGACAAGCGGATTCTAC 505
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 PheAspProValThrPheLeuThrPheProGluGlnLeuAlaArgAsnGlyPheTyr 100

Qy  506 TACCTCGGTCGCGGCGACGAAGTGTGTCGTGTTCGCTTTCGTTGTAAGGTAGAAATTATGAGGTGG 565
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  101 TyrLeuGlyArgGlyAspGluValCysArgValArgPheCysLysLysValGluIleMetArgTrp 120

Qy  566 GTCGAAGGGCGACGATCCTCGCGGCCGATCATCGGAGATGGGCGCGCCCCAGTGTCCCTTTGTA 625
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Db  121 ValGluGlyUspAspProAlaAlaAspHisArgArgTrpAlaArgProGlnCysProPheVal 140

Qy  626 CGAAAAACAAATGTATGCCAACGCTGGGGGAGAGAGGGGAGGAGACGACGCGGTAGAGACGAAATGT 685
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Db  141 ArgLysGlnMetTyrAlaAsnAlaGlyGlyGlyAlaThrAlaValGlyArgAspGluCys 160

Qy  686 GGGGCCAGTGCGCGGCCACGAGCCCCGCCCATGCCCCGCCCGTTGCACGCGGGGTACTCC 745
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Db  161 GlyAlaSerAlaAlaThrGlnProProAlaGlyMetProGlyProValHisAlaArgTyrSer 180

Qy  746 ACCGAAGGGCCGCGCGGGCCTCCCACCTTCAAGGACTTGGGCCCGAGACGTATGGGCCCAAAAACCC 805
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Db  181 ThrGluGlyAlaArgGlyLeuAlaThrPheLysAspTrpProArgArgMetArgGlnLysAspPro 200

Qy  806 GAGGAAACTGGCAGGAGGCCCCGGATTCTTCTATACAGGCCAAGGGTGACAAAAACGAAATGCTTC 865
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Db  201 GluGlnLeuAlaGluAlaAspGlyPheTyrThrGlyGlnGlyAspLysAsnGluMetLeuLys 220

Qy  866 TAATGGCGACGGCAGGGCCTAAAAAGATTGGGAAGCGGATGACGTTCCCGTGGGGAACAGCACGGC 925
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Db  221 TyrCysAspGlyLeuGlyLeuLysAspTrpGluSerAspAspValProTrpGluGlnHisAla 240

Qy  926 AGATGGGTTCGACCCGGCCCGTACGTGCAATTGGTGAAAGGACGGTACTACATTCAGGAG 985
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Db  241 ArgTrpPheAspProArgCysPheAlaTyrValGlnLeuValGlyLysArgAspProValSer 260

Qy  986 GTGAAGTTCGGAGGCCCACTGCGATATCTGCTAGGCGAAGAAGAACAGGGCCCCCACCAAATGAT 1045
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Db  261 ValLysSerGlyAlaThrAlaIleSerAlaSerAlaGlyIleLeuAlaLeuThrLysAsnAsp 280

Qy 1046 TCGACTTAAGAACGTCGCCCAAGAGAGGGCGGAGAAACATTTGGATGACTCTAAAAATATGTAAA 1105
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  281 SerThrLysAsnValAlaGlnGlyLeuGlyLysHisLeuAspAspSerLysIleCysLys 300

Qy 1106 ATATGTTATTCCGAGGAGAGGTAACGTGTGCTTCGTCGCGTGCGCGGCCCAGTGGTGGCGTGC 1165
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 IleCysTyrSerGluArgGluIleArgAsnValCysPheValProPheValProCysGlyHisValValValAlaCys 320

Qy 1166 GCCAAGTGGCGCCGCTGCTCGACGGACGCAAGAGTCGCCCCGATCGTGTCGCGACGAACGTTCACGTTGTGGTAGCGTGC 1225
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321 AlaLysCysAlaLeuSerThrAspLysCysCysGluProMetCysSerArgArgArgThrPheThrArgAsnAla 340

Qy 1226 GTGCGCGCCTTACTTCTCG 1243
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Db  341 ValArgLeuThrPheSer 346
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RESULT 2
US-09-201-936-12

; Sequence 12, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Cydia pomonella
US-09-201-936-12

Alignment Scores:
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Pred. No.:              1.64e-80      Length:        275
Score:                  966.00        Matches:       171
Percent Similarity:     72.66%        Conservative:  39
Best Local Similarity:  59.17%        Mismatches:    55
Query Match:            14.44%        Indels:        24
DB:                     9             Gaps:          3
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US-10-041-859-1 (1-3773) x US-09-201-936-12 (1-275)

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Qy  407 ATGCCCGACATGGCTCGTGTCGAAGAGGAACGTCTCAAAACATTTGATCAGTGGCCCGTTACG 466
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Db    1 MetSerAspLeuArgLeuGluGluGluArgLeuLysThrPheAspGlnTrpProValSer 20

Qy  467 TTTTTTGACCCGGAACAATTGGCCCGACAAGCGGATTCTACTACCTCGGTCGCGGCGACGAA 526
        |||||:::||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 PheLeuSerProGluThrMetAlaLysAsnGlyPheTyrTyrLeuGlyArgSerAspGlu 40

Qy  527 GTGTGTCGTGTTCGCTTTCGTTGTAAGGTAGAAATTATGAGGTGGGTCGAGGCGACGATCCTGCC 586
        ||||||||| ||||:||||||||||||||||||||||||||:::||||||||||||||||
Db   41 ValCysArgCysAlaPheCysLysLysValGluIleMetArgTrpLysGluGlyAspAspProAla 60

Qy  587 GCCGATCATCGGAGATGGGCGCGCCCCAGTGTCCCTTTGTACGAAAAACAAATGTATGCCAAC 646
        |||||||||||||||||||||||||||||||||||||||:::::||||||||||||||
Db   61 AlaAspHisArgTrpAlaProGlnCysProPheVal----------ArgLysGlnMetTyrAlaAsn 74

Qy  647 GCTGGGGGAGGAGGCGCACCGGCTGTCGGTAGGAGACGAAATGTGGGGCCAGTGCCGCGCAG 706
        |||:::||||||||||||||||||||||||||||||||||||||
Db   75 ------------------GlyIleAspValCysGlySerIleValThrThrAsn 86

Qy  707 ------------------CCTCCCCGGCCATGCCCCGGCCCGCTGCACGCGGGTACTCC 745
        :::::||||||| :::||:||:::
Db ......
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OM nucleic - protein search, using frame_plus_n2p model

Copyright (c) 1993 - 2005 Compugen Ltd.

GenCore version 5.1.6

Run on: January 6, 2005, 19:48:41

Title: US-10-041-859-1
Perfect score: 6692
Sequence: 1 cattattaaaccacctcac..........tgcgggctctacttcctgtga 3773

Scoring table: BLOSUM62
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                  Ygapop   10.0 , Ygapext 0.5
                  Fgapop   6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 478139 seqs, 66318000 residues
                  Listing first 45 summaries

Post-processing: Minimum Match 0%
                  Maximum Match 100%

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters: 956278

Command line parameters:
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-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10041859 @CGN_1_1_100 @runat_06012005_133736_3114 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_AA:*
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                  4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                  5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1319	19.7	377	4	US-09-502-528-3	Sequence 3, Appli
2	966	14.4	275	2	US-08-511-485-12	Sequence 12, Appl
3	966	14.4	275	3	US-08-836-134-21	Sequence 21, Appl
4	966	14.4	275	4	US-09-493-784-21	Sequence 21, Appl
5	966	14.4	275	4	US-09-201-936-12	Sequence 12, Appl
6	966	14.4	275	4	US-09-011-356-12	Sequence 12, Appl
7	966	14.4	275	4	US-09-201-932-12	Sequence 12, Appl
8	966	12.9	268	3	US-08-836-134-22	Sequence 22, Appl
9	862	12.9	268	4	US-09-493-784-22	Sequence 22, Appl
10	725.5	10.8	438	4	US-09-586-305A-12	Sequence 12, Appl
11	723.5	10.8	438	4	US-09-586-305A-11	Sequence 11, Appl
12	723.5	10.8	438	4	US-09-586-305A-13	Sequence 13, Appl
13	717.5	10.7	438	4	US-09-586-305A-14	Sequence 14, Appl
14	717.5	10.7	438	4	US-09-586-305A-15	Sequence 15, Appl
15	715.5	10.7	438	4	US-09-586-305A-19	Sequence 19, Appl
16	713.5	10.7	438	4	US-09-586-305A-20	Sequence 20, Appl
17	712.5	10.6	438	4	US-09-586-305A-16	Sequence 16, Appl
18	712.5	10.6	438	4	US-09-586-305A-17	Sequence 17, Appl
19	560.5	8.4	431	4	US-09-586-305A-18	Sequence 18, Appl
20	526.5	7.9	604	5	US-09-569-749-4	Sequence 4, Appli
21	526.5	7.9	604	5	PCT-US96-12860-4	Sequence 4, Appli
22	525.5	7.9	600	3	US-09-212-971-12	Sequence 12, Appl
23	525.5	7.9	600	3	US-08-800-929A-12	Sequence 12, Appl
24	525.5	7.9	604	3	US-09-617-053A-12	Sequence 12, Appl
25	524.5	7.8	604	2	US-08-511-485-6	Sequence 6, Appli
26	524.5	7.8	604	3	US-08-836-134-6	Sequence 6, Appli
27	524.5	7.8	604	3	US-09-617-053A-6	Sequence 6, Appli
28	524.5	7.8	604	3	US-09-617-053A-6	Sequence 6, Appli
29	524.5	7.8	604	4	US-09-201-936-6	Sequence 6, Appli
30	524.5	7.8	604	4	US-09-011-356-6	Sequence 6, Appli
31	524.5	7.8	604	4	US-09-672-717-221	Sequence 221, App
32	524.5	7.8	604	4	US-09-201-932-6	Sequence 6, Appli
33	517.5	7.8	604	4	US-09-201-936-40	Sequence 40, Appl
34	517.5	7.7	602	4	US-09-011-356-40	Sequence 40, Appl
35	517.5	7.7	602	4	US-09-672-717-227	Sequence 227, App
36	517.5	7.7	602	4	US-09-201-932-40	Sequence 40, Appl
37	507.5	7.6	618	2	US-08-511-485-8	Sequence 8, Appli
38	507.5	7.6	618	3	US-09-212-971-8	Sequence 8, Appli
39	507.5	7.6	618	3	US-08-800-929A-8	Sequence 8, Appli
40	507.5	7.6	618	3	US-09-617-053A-8	Sequence 8, Appli
41	507.5	7.6	618	4	US-09-201-936-8	Sequence 8, Appli
42	507.5	7.6	618	4	US-09-011-356-8	Sequence 8, Appli
43	507.5	7.6	618	4	US-09-672-717-223	Sequence 223, App
44	507.5	7.6	618	4	US-09-201-932-8	Sequence 8, Appli
45	501	7.5	497	4	US-08-657-759-1	Sequence 1, Appl

; Search time 86.5 Seconds
; (without alignments)
; 5785.383 Million cell updates/sec

ALIGNMENTS

RESULT 1
US-09-502-528-3
; Sequence 3, Application US/09502528
; Patent No. 6570069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibitors of Apoptosis
; FILE REFERENCE: 023070-112000US
; CURRENT APPLICATION NUMBER: US/09/502,528
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 3
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Spodoptera frugiperda
; FEATURE:
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SfIAP)
US-09-502-528-3

Alignment Scores:
Pred. No.:   5.16e-132
Score: 1319.00
Percent Similarity: 78.80%
Best Local Similarity: 67.66%
Query Match: 19.71%

                        Length: 377
                        Matches: 249
                        Conservative: 41
                        Mismatches: 60
                        Indels: 18
                        Gaps: 7

US-10-041-859-1 (1-3773) x US-09-502-528-3 (1-377)

Qy   188 AAAAGGAAAAATATACCAAATGAGTTGACGAAAGTTGCTAAAAATGAGCTGCCGCACG 247
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Db   188 AAAAGGAAAAATATACCAAATGAGTTGACGAAAGTTGCTAAAAATGAGCTGCCGCACG 247

RESULT 2

US-08-511-485-12
; Sequence 12, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-12

Alignment Scores:
Pred. No.:   2.62e-94   Length: 275
Score: 966.00   Matches: 171
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Best Local Similarity: 59.17%   Mismatches: 55
Query Match: 14.44%   Indels: 24
DB: 2   Gaps: 3

US-10-041-859-1 (1-3773) x US-08-511-485-12 (1-275)

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Db      1 MetSerAspLeuArgLeuGluGluSerGlyLeuLysValArgArgLeuAsnThrPheGluGlyLysTrpProValSer 20

Qy    467 TTTTTGACGCCGGAACAAATTGGCCCCGACAACGGAATTCTACTACCTTCGGGTCGCGGACGAA 526
          |||::|                 ||||:::            ::|::|||||||   |||
Db     21 PheLeuSerProGluThrMetAlaLysAsnGlyPheTyrTyrLeuGlyArgSerAspGlu 40

Qy    527 GTGTGCGTTGCTTTTCTGTAAGGTAGAGAAATTATGAGGTGGGGTGGGGACGAATCCTGCC 586
          |||   ||||::            :::||||||||||||||         |||::|
Db     41 ValArgCysAlaPheCysGlyValGluIleMetArgTrpLysSerGlyAspProAla 60

Qy    587 GCCGATCATCGGAGATGGGGCGCCCCCAGTGTCCCTTTGTACGGAAAACAAAATGTATGCCAAC 646
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Db     61 AlaAspHisGlyLysHisTrpAlaProGlnCysProPheValLys------ 74

Qy    647 GCTGGGGGAGGAGGCGACCGCCGCTGTCGGTAGAGACGAATGTGGGGGCGCCCAGTGCGCGGCCGCGGCAG 706
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          :::||| |||:::          |||||||||||||||::||:::|:::::|||||:::|||
Db     32 LeuThrLeuPheLysSerGlySerLeuGlyAlaLysIleArgPro---LeuAlaProLeu 50

Qy    305 ATGTTA------TCCTCCGTGGTGAGTCTTCAACGACATCCACACTCCCGTCACCTTCGTCG 358
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Db     51 MetLeuProThrProSerTyrAspSerAsnAlaGlySerProSerLeuSerProSerThr 70

Qy    359 -----------TCAGCTGATAAAACGGATAATCACGACACATTCAACTTC 397
                     :::|||||||:::|||||::::::|||:::|||||:::|||
Db     71 ProCysSerSerSerPheSerIleAlaSpLysThrAspAsnHisAspThrPheGlyPhe 90

Qy    398 CTTCCTGGATATGCCCGACATGGCTCGTTGCTGAGAGGAACGTCTGAAAACATTTGATCAGTGG 457
          |||    :::|||   :::|||||:::         ||||||||||||||||:::|:::||:::
Db     91 SerAlaAspThrValAspMetAlaArgLysGluArgMetLysThrPheGlyLysTrp 110

Qy    458 CCCGTTACGTTTTTTGACGCCGGAACAAATTGGCCCCGACGGATTCTACTACCTTCGGGTCGC 517
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Db    111 ProValSerProPheLeuSerGlyGluGlnIleLeuAlaArgAsnGlyPheTyrTyrLeuGlyArg 130

Qy    518 GGCGACGAAGTGTGCGTTGCTTTCTGTAAGGTAGAAAATTATGAGGTGGGTTCGAAGGCGAC 577
          |||||||||||||   ||||:::            :::||||||||||         |||
Db    131 ArgAspGluAlaCysGlyAlaPheCysLysValGluIleMetArgTrpValGluGlyAsp 150

Qy    578 GATCCTGCCGCCGATCATCGGAGATGGGGCGCCCCAGTGTCCCTTTGTACGGAAAAACAAATG 637
          |||:::|||:::|||||:||||||||         |||||||||||||||:::  :::  :::
Db    151 AspProAlaAlaAspHisGlnAsnArgTrpAlaProGlnCysProPheValArgLys---Leu 169

Qy    638 TATGCCAACGCTGGGGGAGGAGGCGACCGGCTGTCCGGTAGAGACGAAATGTGGGGCGCCCAGTGCG 697
          |||:::      |||      ||||||:::||||||:::           |||:::
Db    170 AsnGlyThrAlaAlaAlaAspThrGlySerSerGlyGlnIleAspGlyLysTyrThrLysGlyGlnAla 189

Qy    698 GCC-------ACCGAGCTTCCCCGCATGCCCACGCGCGGGGTACTTCCACC 748
          |||       :::                ::|:::   |||
Db    190 AlaProSerGlyThrSerProProArgMetLeuAlaGlyProValHisProArgTyrAlaSer 209

Qy    749 GAGCCGCCGCCGGGCTTCGCCACCTTCAAGGACTGGGCCGAGACGTATCGCCCAAAAACCCGAG 808
          ||||||:::|||||||:::   ::|:::   ||||||:::|||:::|||:::|||:::
Db    210 GluAlaAlaAlaArgLeuArgSerPheLysAspTrpProArgCysMetAspArgGlnLysSerProGlu 229

Qy    809 GAACTGGCAGAGGCCGGAGTTCTTCTATACAGGCCAAAGGTGACAAAACGCTTCTAT 868
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Db    230 GluLeuAlaGluAlaGlyPhePhePheTyrThrGlyGlnTyrValAspAspCysPhePheTyr 249

Qy    869 TGGGACGCGGAGGGGCTAAAAGATTGGGAAAGCGGATGACGTTCCGTGGGACACAGCACGCCAGA 928
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Db    250 CysAspGlyGlyLeuLysAspTrpGluAsnHisAspValProTrpGluGlnHisAlaArg 269

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Db    270 TrpPheAspArgCysAlaTyrArgValGlnLeuValLysGlyTyrValGlnLysVal 289

Qy    989 AAGTCGGGAGGCCACTGCGATATCTGCTAGGCGAAGAGAACAG------GCCGCCACC 1039
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Db    310 ThrArgLeuGluProSerProProAlaGluValAlaProGluAsnSerValAlaProSerLysSerLeu 329

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Qy   1160 GCCGTGAGCGCCAAGTACCGGCGCTGTCGACGGACAAGTGCCCGATTGTGTCGGAAGGGTTCACG 1219
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Db    350 AlaCysGlyAlaLysCysAlaLeuLeuAlaAspHisLysCysProMetCysArgGlnThrPheGln 369

Qy   1220 AATGCGGTGCGCGGCCTCTACTTCTCG 1243
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Db    370 AsnAlaValArgGlyLeuTyrPheSer 377
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QM nucleic - protein search, using frame_plus_n2p model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:　　January 6, 2005, 19:58:08 ; Search time 444.5 Seconds
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　　　　　　　　　　　　　　　　　　　　6089.924 Million cell updates/sec

Title:　　　　US-10-041-859-1
Perfect score: 6692
Sequence:　　1 cattattaaactccacttcac...........tgcggcctacttctcgtga 3773

Searched:　　2002273 seqs, 358729299 residues
　　　　　　　　Listing first 45 summaries

Scoring table: BLOSUM62
　　　　　　　　Xgapop 10.0 , Xgapext　0.5
　　　　　　　　Ygapop 10.0 , Ygapext　0.5
　　　　　　　　Fgapop　6.0 , Fgapext　7.0
　　　　　　　　Delop　6.0 , Delext　7.0

Total number of hits satisfying chosen parameters:　　4004546

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
　　　　　　　　　Maximum Match 100%

Command line parameters: -DEV=xlp
-MODEL=frame+_n2p.model
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-DB=A_Geneseq_23Sep04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000000
-USER=US10041859 @CGN_1_1_552 @runat_06012005_133739_3178 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :　　A_Geneseq_23Sep04:*
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　　　　　　2: geneseqp1990s:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	1887	28.2	346	5	ABB78046	Amino aci
2	1319	19.7	377	7	AAE07881	Fall army
3	767.5	11.5	263	5	ABB09488	AmEPV bac
4	721.5	10.8	438	4	AAB48189	Drosophil
5	719.5	10.8	438	4	AAB48189	Drosophil
6	719.5	10.8	438	4	ABB61858	Drosophil
7	719.5	10.8	438	4	Abb67347	Drosophil
8	719.5	10.8	438	4	AAB48188	Drosophil
9	719.5	10.8	438	8	AAB48190	Drosophil
10	713.5	10.7	438	4	AAB48192	Drosophil

ALIGNMENTS

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14	708.5	10.6	438	4	AAB48193	Drosophil
15	708.5	10.6	438	4	AAB48194	Drosophil
16	576.5	8.6	434	4	AAB48195	Drosophil
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18	526.5	7.9	604	2	AAW13546	Human c-I
19	526.5	7.9	604	2	AAY52703	Human cel
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21	526.5	7.9	604	6	ABU07431	Protein d
22	526.5	7.9	604	7	ADB80948	Human CIA
23	526.5	7.9	604	8	Aae39811	Human cel
24	526.5	7.9	604	7	Adg87135	Human CIA
25	526.5	7.9	604	8	Adh74643	Human CIA
26	526.5	7.9	600	2	Aaw69298	Murine HI
27	525.5	7.9	604	6	ABp72155	Mouse inh
28	525.5	7.9	604	2	AAw19582	Human apo
29	524.5	7.8	604	2	AAw69295	Human HIA
30	524.5	7.8	604	5	Abg65664	Human inh
31	524.5	7.8	602	5	Abg65667	Mouse inh
32	517.5	7.7	602	2	ABp72160	Mouse apo
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34	507.5	7.6	618	2	AAw19583	Human inh
35	507.5	7.6	618	5	Aaw69296	Human HIA
36	507.	7.6	618	5	Abg65665	Human inh
37	501	7.5	618	5	Adi39803	Drosophil
38	500.5	7.5	496	2	AAw19745	Mouse inh
39	500.5	7.5	618	2	AAw19746	Human inh
40	500.5	7.5	618	2	Aaw13545	Human c-I
41	500.5	7.5	618	2	Aay33998	Human cel
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45	500.5	7.5	618	7	Add25639	Binding d

RESULT 1
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AC　　ABB78046;
ID　　ABB78046 standard; protein; 346 AA.
DT　　22-OCT-2002　(first entry)
DE　　Amino acid sequence of inhibitor of apoptosis protein BmIAP.
KW　　Inhibitor of apoptosis protein; IAP; BmIAP; silkworm; apoptosis; insect;
KW　　Spodoptera frugiperda; insult-resistant plant; caspase.
OS　　Bombyx mori.

FH	Key	Location/Qualifiers
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FT		/note= "BIR domain 1"
FT	Domain	182..249
FT		/note= "BIR domain 2"
FT	Domain	298..314
FT		/note= "RING domain"

PN　　WO0202535586-A2.
PD　　11-JUL-2002.
PF　　07-JAN-2002; 2002WO-US000314.
PR　　08-JAN-2001; 2001US-02604787P.
PA　　(BURN-) BURNHAM INST.
PI　　Maeda S, Huang Q, Reed JC, Deveraux QL;

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XX
DR     WPI; 2002-590628/63.
DR     N-PSDB; ABQ78228.
XX
PT     Novel recombinant polypeptide, inhibitor of apoptosis protein family
PT     member BmIAP from silkworm Bombyx mori BmN cells, useful for inhibiting
PT     apoptosis and identifying an agent that modulates activity of
PT     polypeptide.
XX
PS     Claim 39; Page 31; 62pp; English.
XX
CC     The present scene represents a polypeptide which is an inhibitor of
CC     apoptosis protein (IAP) family member, and designated BmIAP. BmIAP is
CC     derived from silkworm Bombyx mori BmN cells. The BmIAP polypeptide
CC     contains two baculoviral IAP repeat (BIR) domains, followed by a RING
CC     domain. BmIAP polypeptides and polynucleotides are useful for inhibiting
CC     apoptosis in insect cells, especially Spodoptera frugiperda or Bombyx
CC     mori cells, and mammalian cells, and plant cells. They are also useful
CC     for generating a biotic or abiotic insult-resistant plant. BmIAP is also
CC     useful for inhibiting caspases
XX
SQ     Sequence 346 AA;
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Alignment Scores:
Pred. No.:
Score:                  2.71e-182
Score:                  1887.00
Percent Similarity:     100.00%
Best Local Similarity:  100.00%
Query Match:            28.20%
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                         Matches:        346
                         Conservative:   0
                         Mismatches:     0
                         Indels:         0
                         Gaps:           0
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US-10-041-859-1 (1-3773) x ABB78046 (1-346)

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Db     1   MetGluLeuThrLysValAlaLysAsnGlyAlaAlaAlaThrLeuValMetLeuLysAsn 20

Qy     266 GCGCGGGATCGAAAAATGCCACCTTTCATTGGTCCGCTCATGTTATCCTCGTGTGAGTGT 325
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21  AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40

Qy     326 TCAACGACATCCACACTCCCGTCACCTTCGTCGTCGTCAGCTGATAAAACGGATAATCACGAC 385
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41  SerThrThrSerThrLeuProSerProSerSerSerAlaLysThrAspAsnHisAsp 60

Qy     386 ACAATCAACTTCCTTCCTGATAATGCCCGACATGGGTCCGTCGTGAAGAGGAAGTCTGAAAACA 445
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Db     61  ThrPheAsnPheLeuProAspMetProAspMetArgArgAspValIleLysThr 80

Qy     446 TTTGATCAGTGGGCCCCGGTTAGGTTTTGAGGCCGGAACAATTGGCCGCGATTCTAC 505
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Db     81  PheAspGlnTrpProValThrPheLeuThrProGlnLeuLeuAlaAlaAsnGlyPheTyr 100

Qy     506 TACCTCGGTTCGCGCGCGACGAAGTGTGCGTGTGCCTTCTGTTAAGGTAGAAAATTATGAGGTGG 565
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101 TyrLeuGlyArgGlyAspGlyValCysGlySAlaPheCysGlyValGlyIleIleMetAsp 120

Qy     566 GTCGAAGGCGACGACGATCCTGCCGCCCGATCATCGGAGATGGGGCGCCCCAGTGTCCCTTGTA 625
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Db     121 ValGluGlyAspAspProAlaLaAspHisArgArgTrpAlaProGlnCysProPheVal 140

Qy     626 CGAAAACAAATGTATGCCAACGCCTGGGGGAGAGGGCGACCGCGTTCGGTAGAGACGAATGT 685
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     141 ArgLysGlnMetTyrAlaAsnAlaGlyGlyGluAlaThrAlaValGlyArgAspGluCys 160

Qy     686 GGGGCCCAGTGCGGCCACCACCGCTTCCCCGCCCCGGTCACGCGCGGTACTCC 745
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Qy     746 ACCGAGGGCCGCGGGCGCGCTGCACCCTTCAAGGACTGCGGCCGAGACGGTAAGAGCAAAACCC 805
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Qy     806 GAGGAACTGGCACGAGAGGCCGGATTCTTCTATACAGCGAGGTGACAAAACGAAATGCTTC 865
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     201 GluGluLeuAlaArgGluAlaGlyPhePheTyrThrGlyHisCysPhe 220

Qy     866 TATTCGACCGGAGGGCGTAAAAGATTGGGAAAAGCCAATGAGAGTTCCGTGGGAACACAGCGCC 925
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     221 TyrCysAspGlyGlyLeuLysAspLeuTrpGluSerArgAspAspValProTrpGluGlnHisAla 240

Qy     926 AGATGGTTCGACCCGCTGCGGTACGTGACGTTCAATTGGTGAAAAGGACGTGACTACATTCAGAG 985
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ArgTrpPheAspProCysAlaTyrValGlnLeuAsnTrpValLysGlyArgAspTyrIleGlyLys 260

Qy     986 GTGAAGTCGGAGGGCGCACTGCGGATATCTGCCTAGGCGAAGAGAGAACAGGCCGCCAAATGAT 1045
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Db     261 ValLysSerGluAlaThrAlaAsnIleAlaLeuGluGluGluArgGluArgGluArgGluValAsp 280

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Db     281 SerThrLysAsnValAlaGlnGluGlyHisLeuLeuAspAspSerLysLysLys 300

Qy     1106 ATATGTTATTCCGAGGAGGGTAACGTTGTGCTTCGTGCTGTGCCTGCGCGCCACCTGGTGTGGCGTGG 1165
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Db     301 IleCysTyrSerGluGluArgAsnValCysPheValProCysGlyHisValValAlaCys 320

Qy     1166 GCCAAGTGCGGCGCTGTCGACAGGACCAAGTGCCCCGATGTGTGCCAGGACAGTTCACGAAGCG 1225
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Qy     1226 GTGCGGGCTCTACTTCTCG 1243
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Db     341 ValArgLeuTyrPheSer 346
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RESULT 2
AAE07881
ID     AAE07881 standard; protein; 377 AA.
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AC     AAE07881;
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DT     01-NOV-2001  (first entry)
XX
DE     Fall armyworm inhibitor of apoptosis (IAP) protein.
XX
KW     Fall armyworm; inhibitor of apoptosis; IAP; transgenic plant;
KW     apoptosis inhibitor; therapy; acquired immune deficiency syndrome; AIDS;
KW     neurodegenerative disease; Alzheimer's disease; aplastic anaemia;
KW     Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;
KW     myelodysplastic syndrome; toxin-induced liver disease; ischaemic injury;
KW     myocardial infarction; stroke; reperfusion injury; cancer; nootropic;
KW     autoimmune disorder; lupus erythematosus; multiple sclerosis; vasotropic;
KW     insecticide; viral infection; anti-HIV; human immunodeficiency virus;
KW     neuroprotective; antianaemic; cardiant; cerebroprotective; vulnerary;
KW     cytostatic; immunosuppressive; virucide; antialcoholic.
XX
OS     Spodoptera frugiperda.
XX
PN     WO200159108-A2.
XX
PD     16-AUG-2001.
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PF     07-FEB-2001; 2001WO-US004071.
XX
PR     10-FEB-2000; 2000US-00502528.
XX
PA     (REGC ) UNIV CALIFORNIA.
PA     (MAED/) MAEDA H.
XX
PI     Maeda S,  Hammock BD,  Huang Q,  Maeda H;
XX
DR     WPI; 2001-514667/56.
DR     N-PSDB; AAD14419.
XX
PT     Novel nucleic acid construct comprising cDNA encoding inhibitor of
PT     apoptosis proteins, useful for controlling apoptosis in target cells and
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QM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on:　　January 13, 2005, 01:23:43 ; Search time 15375 Seconds
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Title:　　　　　US-10-041-859-1
Perfect score:　3773
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Scoring table:　IDENTITY_NUC
　　　　　　　　　Gapop 10.0 , Gapext 1.0
Searched:　　　4526729 seqs, 2364849745 residues
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
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Database :　　　GenEmbl1:*
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　　　　　　　12: gb_sy:*
　　　　　　　13: gb_un:*
　　　　　　　14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3773	100.0	3773	6	AX664311	AX664311 Sequence
2	2716	72.0	2716	3	AF281073	AF281073 Bombyx mo
3	1033	27.4	1041	3	AY155274	AY155274 Bombyx mo
4	441.8	11.7	1739	3	AF186378	AF186378 Spodopter
5	441.8	11.7	1739	6	AR340174	AR340174 Sequence
6	441.8	11.7	1739	6	AX213188	AX213188 Sequence
7	437.2	11.6	1134	6	AR340175	AR340175 Sequence
8	437.2	11.6	1134	6	AX213189	AX213189 Sequence
9	433.2	11.5	2614	3	AF195528	AF195528 Trichoplu
10	292.8	7.8	123500	14	U53466	U53466 Cydia pomon
11	270	7.2	1247	14	AY525121	AY525121 Anticarsi
12	254	6.7	1032	14	U82510	U82510 Choristoneu
13	254	6.7	129609	14	AF512031	AF512031 Choriston
14	226.6	6.0	1386	14	NPHIAP	NPHIAP
15	226.6	6.0	13995	14	OPU75930	U75930 Orgyia pseu
16	226.2	6.0	3248	14	AF045936	AF045936 Buzura su
17	218.6	5.8	131158	14	AY327402	AY327402 Choriston
18	208.2	5.5	1241	14	AB088850	AB088850 Hyphantri
19	200.6	5.3	1787	14	AF180757	AF180757 Epiphyas
20	200.6	5.3	1787	14	AY042265	AY042265 Epiphyas
21	161	4.3	110907	14	AY229987	AY229987 Cryptcphl
22	142.4	3.8	50000	6	AX392733	AX392733 Sequence
23	142.4	3.8	232392	14	AF250284	AF250284 Amsacta m
24	130.4	3.5	794	6	AX392714	AX392714 Sequence
25	130	3.4	113220	14	AP006270	AP006270 Adoxophye
26	120.6	3.2	158611	14	AF169823	AF169823 Spodopter
27	115	3.0	158482	14	AY126275	AY126275 Mamestra
28	112.4	3.0	133877	14	AC120883	AC120883 Homo sapi
29	111.8	3.0	8056	6	AX599046	AX599046 Sequence
30	110.8	2.9	67970	6	PFMALIP3	AL031746 Plasmodiu
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32	109.8	2.9	258658	3	AE014832	AE014832 Plasmodiu
33	109.8	2.9	135121	9	AC069525	AC069525 Homo sapi
34	109	2.9	348174	3	CR382399	CR382399 Plasmodiu
35	108.2	2.9	67970	3	PFMALIP3	AL031746 Plasmodiu
36	108	2.9	86826	3	PFMAL3P5	AL034556 Plasmodiu
37	107	2.8	4601	3	DMU11584	U11584 Drosophila
38	106.4	2.8	4601	3	DMU11584	U11584 Drosophila
39	106.4	2.8	19517	3	DMU37541	U37541 Drosophila
40	106.2	2.8	1662	3	AF447592	AF447592 Ochlerota
41	105.8	2.8	254050	3	PFA929358	PFA929358 Plasmodiu
42	105.4	2.8	4601	3	DMU11584	U11584 Drosophila
43	105.4	2.8	19517	3	DMU37541	U37541 Drosophila
44	105.2	2.8	347751	3	PFMAL4P3	AL035476 Plasmodiu
45	104.8	2.8	163735	9	AC027277	AC027277 Homo sapi

ALIGNMENTS

RESULT 1
AX664311

LOCUS	AX664311	3773 bp	DNA	linear	PAT	22-MAR-2003

DEFINITION　Sequence 1 from Patent WO02053586.
ACCESSION　　AX664311
VERSION　　　AX664311.1　GI:29164241
KEYWORDS　　.
SOURCE　　　　Bombyx mori (domestic silkworm)
　ORGANISM　　Bombyx mori
　　　　　　　Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
　　　　　　　Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
　　　　　　　Bombycoidea; Bombycidae; Bombyx.
REFERENCE　　1
　AUTHORS　　Huang,Q., Reed,J.C., Deveraux,Q.L. and Maeda,S.D.
　TITLE　　　Inhibitor of apoptosis proteins and nucleic acids and methods for
　　　　　　　making and using them
　JOURNAL　　Patent: WO 02053586-A 1 11-JUL-2002;
　　　　　　　The Burnham Institute (US)
FEATURES　　　　　　　　　Location/Qualifiers
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ORIGIN

Qy

Query Match	100.0%;	Score 3773;	DB 6;	Length 3773;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3773;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy　　1 CATTATTATTAAACTCACTTCACTTCGGTAGTGTGAAGTTAACGTAGAATGTTAACCTCCGCGGCTCTTC 60

This page contains a DNA sequence alignment printout with paired rows labeled "Qy" (query) and "Db" (database), showing nucleotide sequences with alignment bars (|||) between them. The alignment spans numbered positions from 1 to approximately 2220, arranged in two columns on the rotated page.

QM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on: January 13, 2005, 09:54:59 ; Search time 5052 Seconds
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                                  3238.764 Million-cell updates/sec

Title: US-10-041-859-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAAATLVMLKN..........TDKCPMCRRTPTNAVRLYFS 346

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Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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       13: gb_un:*
       14: gb_vi:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1887	100.0	2716	3	AF281073	AF281073 Bombyx mo
2	1887	100.0	3773	9	AX664311	AX664311 Sequence
3	1866	98.9	1041	3	AY155274	AY155274 Bombyx mo
4	1327	70.3	2614	3	AF195528	AF195528 Trichoplu

ALIGNMENTS

5	1311	69.5	1134	6	AR340175	AR340175 Sequence
6	1311	69.5	1134	6	AX213189	AX213189 Sequence
7	1311	69.5	1739	6	AF186378	AF186378 Spodopter
8	1311	69.5	1739	3	AR340174	AR340174 Choriston
9	1311	69.5	1739	6	AX213188	AX213188 Sequence
10	966	51.2	122500	14	U53466	U53466 Cydia pomon
11	937	49.7	1247	14	AY525121	AY525121 Anticarsi
12	890.5	47.2	131158	14	AY327402	AY327402 Choriston
13	879	46.6	1241	14	AB088850	AB088850 Hyphantri
14	879	46.6	129609	14	AF512031	AF512031 Choriston
15	876	46.4	1032	14	CFU82510	U82510 Christoneu
16	873	46.3	1787	14	AF180757	AF180757 Epiphyas
17	873	46.3	3248	14	AF045936	AF045936 Buzura su
18	873	46.3	11854	14	AY043265	AY043265 Epiphyas
19	862	45.7	1386	14	NPHIAP	L22564 Orgyia pseu
20	862	45.7	131995	14	OPU75930	U75930 Orgyia pseu
21	787	41.7	50000	6	AX392733	AX392733 Sequence
22	787	41.7	232392	14	AF250284	AF250284 Amsacta m
23	748	39.6	794	6	AX392714	AX392714 Sequence
24	747.5	39.6	110907	14	AY229987	AY229987 Cryptophl
25	728	38.6	135611	14	AF169823	AF169823 Spodopter
26	725.5	38.4	14250	6	AR432086	AR432086 Sequence
27	723.5	38.3	1317	6	AR432085	AR432085 Sequence
28	723.5	38.3	1317	6	AR432087	AR432087 Sequence
29	723.5	38.3	2017	3	DRODIAP1X	L49440 Drosophila
30	719.5	38.1	1858	6	CQ601074	CQ601074 Sequence
31	719.5	38.1	2013	6	CQ584607	CQ584607 Sequence
32	719.5	38.1	10432	6	CQ584606	CQ584606 Sequence
33	719.5	38.1	14250	6	CQ601073	CQ601073 Sequence
34	719.5	38.1	85633	2	AC014423	AC014423 Drosophil
35	719.5	38.1	169209	3	AC093499	AC093499 Drosophil
36	719.5	38.1	176056	3	AC010066	AC010066 Drosophil
37	719.5	38.1	283815	3	AE003528	AE003528 Drosophil
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43	712.5	37.8	1317	6	AR432091	AR432091 Sequence
44	712	37.7	1662	3	AF447592	AF447592 Ochlerota
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RESULT 1
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LOCUS   AF281073   2716 bp   mRNA   linear   INV 30-MAY-2001
DEFINITION   Bombyx mori inhibitor of apoptosis protein (IAP) mRNA, complete
             cds.
ACCESSION   AF281073
VERSION   AF281073.1 GI:14248545
KEYWORDS   .
SOURCE   Bombyx mori (domestic silkworm)
  ORGANISM   Bombyx mori
             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
             Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
             Bombycoidea; Bombycidae; Bombyx.
REFERENCE   1 (bases 1 to 2716)
  AUTHORS   Huang,Q., Deveraux,Q.L., Maeda,S., Stennicke,H.R., Hammock,B.D. and
             Reed,J.C.
  TITLE   Cloning and characterization of an inhibitor of apoptosis protein
             (IAP) from Bombyx mori
  JOURNAL   Biochim. Biophys. Acta 1499 (3), 191-198 (2001)
  PUBMED   11341966
REFERENCE   2 (bases 1 to 2716)
  AUTHORS   Huang,Q., Deveraux,Q.L., Maeda,S., Salvesen,G.S., Stennicke,H.R.,
             Hammock,B.D. and Reed,J.C.
  TITLE   Direct Submission
  JOURNAL   Submitted (21-JUN-2000) Entomology, University of California at
             Davis, One Shields Avenue, Davis, CA 95616, USA
FEATURES   Location/Qualifiers

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ORIGIN

US-10-041-859-2 (1-346) x AF281073 (1-2716)

Alignment Scores:
Pred. No.:   1
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Percent Similarity: 1887.00   Matches: 346
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 3   Indels: 0
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Qy   1 MetGluLeuThrLysValAlaAlaLysAsnGlyAlaAlaAlaThrLeuValMetLeuLysAsn 20
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Db   326 TCAACGACAATCCAACACTCCCGTCACCTTCGTCAGCTGAAAAGGATAATCACGAC 385

Qy   61 ThrPheAsnPheLeuProAspMetProAspMetArgArgGluGluGluArgLeuLysThr 80
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Qy   81 PheAspGlnTrpProValThrPheLeuThrProGluGlnLeuAlaArgAsnGlyPheTyr 100
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Qy   201 GluGluLeuAlaGluAlaGlyPhePheTyrThrGlyGlnGlyAspLysThrLysCysPhe 220
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Qy   221 TyrCysAspGlyGlyLeuLysAspTrpGluSerAspAspValProTrpGluGlnHisAla 240
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Db   926 AGATGGTTCGACCGCTGCGCGTACGTGCAATTGGTAAAAGGACGTGACTACATTCAGAAG 985

Qy   261 ValLysSerGluAlaThrAlaIleSerAlaSerGluGluGluGlnAlaAlaThrAsnAsp 280
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Db   1046 TCGACTAAGAACGTCGCCCAAGAGGGCGAGAAACATTTGGATGACTCTAAAAATGTAAA 1105

Qy   301 IleCysTyrSerGluGluArgAsnValCysPheValProCysGlyHisValValAlaCys 320
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Db   1106 ATATGTTATTCCGAGGAGCGGTAACGTGTGCTTCGTGCCGTGCGGCCACGGTGGTCGGTGC 1165

Qy   321 AlaLysCysAlaLeuSerThrAspLysCysProMetCysArgArgThrPheThrAsnAla 340
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Db   1166 GCCAAGTGCGCCCTGTCGACGGACAAGTGCCCGATGTGTCGCAGGACGTTCACGAATGCG 1225

Qy   341 ValArgLeuTyrPheSer 346
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Db   1226 GTGCGGCTCTACTTCTCG 1243

RESULT 2
AX664311
LOCUS   AX664311   3773 bp   DNA   linear   PAT 22-MAR-2003
DEFINITION   Sequence 1 from Patent WO2053586.
ACCESSION   AX664311
VERSION   AX664311.1   GI:29164241
KEYWORDS   .
SOURCE   Bombyx mori (domestic silkworm)
ORGANISM   Bombyx mori
     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
     Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
     Bombycoidea; Bombycidae; Bombyx.
REFERENCE   1
AUTHORS   Huang,Q., Reed,J.C., Deveraux,Q.L. and Maeda,S.D.
TITLE   Inhibitor of apoptosis proteins and nucleic acids and methods for
     making and using them
JOURNAL   Patent: WO 02053586-A 1 11-JUL-2002;
     The Burnham Institute (US)
FEATURES   Location/Qualifiers
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RTFTNAVRLYFS"

ORIGIN

Alignment Scores:
Pred. No.:   1
Score: 8.48e-133   Length: 3773
Percent Similarity: 1887.00   Matches: 346
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
     Indels: 0